



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 181717

TO: Minh-Tam Davis
Location: REM-3A24&3C18
Art Unit: 1642
Thursday, March 09, 2006

Case Serial Number: 10/001469

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

181717

From: Chan, Christina
Sent: Wednesday, March 08, 2006 2:25 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 10/001469

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

CRFE

-----Original Message-----

From: Davis, Minh-Tam
Sent: Wednesday, March 08, 2006 11:19 AM
To: Chan, Christina
Subject: Rush search request for 10/001469

Please search in commercial database, issued patent files, PGPUB and interference:
The protein of SEQ ID NO:2866
Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

4

Point of Contact:
Alexandra Wacławiw
Technical Info. Specialist

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:21.49 ; Search time 186 Seconds

(without alignments)
751.196 Million cell updates/sec

Title: US-10-001-469A-2866

Perfect score: 1622
Sequence: 1 MWVDPNGNSATYFILGL.....KEIRQRILRFVYATASRP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21:*

1: geneseqp19808:*

2: geneseqp19808:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20038:*

8: geneseqp20048:*

9: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1622	100.0	318	7	AD109914 Optimised
2	1622	100.0	318	7	AD109880 101P3A11
3	1622	100.0	318	7	AD109871 101P3A11
4	1622	100.0	338	7	AD109912 Optimised
5	1619	99.8	318	3	AAV92365 G-protein
6	1619	99.8	318	4	AAW01306 P835P anti
7	1619	99.8	318	4	AAU69951 Human pro
8	1619	99.8	318	4	AAU69951 Human pro
9	1619	99.8	318	4	AAU69951 Human pro
10	1619	99.8	318	4	AAU69951 Human pro
11	1619	99.8	318	4	AAU69951 Human pro
12	1619	99.8	318	4	AAU69951 Human pro
13	1619	99.8	318	4	AAU69951 Human pro
14	1619	99.8	318	4	AAU69951 Human pro
15	1619	99.8	318	4	AAU69951 Human pro
16	1619	99.8	318	4	AAU69951 Human pro
17	1619	99.8	318	4	AAU69951 Human pro
18	1619	99.8	318	4	AAU69951 Human pro
19	1619	99.8	318	4	AAU69951 Human pro
20	1619	99.8	318	4	AAU69951 Human pro
21	1619	99.8	318	4	AAU69951 Human pro
22	1619	99.8	318	4	AAU69951 Human pro
23	1619	99.8	318	4	AAU69951 Human pro
24	1619	99.8	318	4	AAU69951 Human pro

25	1619	99.8	318	8	AD030402
26	1619	99.8	318	8	AD098144
27	1617	99.7	317	4	AB85002
28	1617	99.7	317	4	AB85002
29	1617	99.7	317	4	AB85002
30	1614	99.5	317	5	AB61886
31	1614	99.5	317	7	AD86293
32	1614	99.5	317	7	AD86293
33	1612	99.4	318	4	AB844535
34	1612	99.4	318	4	AB844535
35	1612	99.4	318	4	AB844535
36	1612	99.4	318	4	AB844535
37	1534	94.6	302	7	AD109903
38	1515	93.3	298	6	AD109904
39	1513	93.3	297	6	AD109904
40	1512	93.2	316	7	AD109908
41	1512	93.2	317	8	AD030422
42	1486	91.6	292	6	AD019531
43	1262	77.8	249	8	ADN58731
44	985	60.7	330	8	AD030425
45	979	60.4	315	4	AA671762
46	979	60.4	318	5	AB668142
47	979	60.4	318	5	AB668142
48	979	60.4	320	4	AAW01175
49	979	60.4	330	4	AAU69820
50	979	60.4	330	4	AAU69820
51	979	60.4	330	4	AAU69820
52	979	60.4	330	4	AAU69820
53	979	60.4	330	4	AAU69820
54	979	60.4	330	4	AAU69820
55	979	60.4	330	4	AAU69820
56	979	60.4	330	4	AAU69820
57	979	60.4	330	4	AAU69820
58	979	60.4	330	4	AAU69820
59	979	60.4	330	4	AAU69820
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61	979	60.4	330	4	AAU69820
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64	979	60.4	330	4	AAU69820
65	979	60.4	330	4	AAU69820
66	979	60.4	330	4	AAU69820
67	979	60.4	330	4	AAU69820
68	979	60.4	330	4	AAU69820
69	979	60.4	330	4	AAU69820
70	979	60.4	330	4	AAU69820
71	979	60.4	330	4	AAU69820
72	979	60.4	330	4	AAU69820
73	979	60.4	330	4	AAU69820
74	979	60.4	330	4	AAU69820
75	979	60.4	330	4	AAU69820
76	979	60.4	330	4	AAU69820
77	979	60.4	330	4	AAU69820
78	979	60.4	330	4	AAU69820
79	979	60.4	330	4	AAU69820
80	979	60.4	330	4	AAU69820
81	979	60.4	330	4	AAU69820
82	979	60.4	330	4	AAU69820
83	979	60.4	330	4	AAU69820
84	979	60.4	330	4	AAU69820
85	979	60.4	330	4	AAU69820
86	979	60.4	330	4	AAU69820
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89	979	60.4	330	4	AAU69820
90	979	60.4	330	4	AAU69820
91	979	60.4	330	4	AAU69820
92	979	60.4	330	4	AAU69820
93	979	60.4	330	4	AAU69820
94	979	60.4	330	4	AAU69820
95	979	60.4	330	4	AAU69820
96	979	60.4	330	4	AAU69820
97	979	60.4	330	4	AAU69820

98 937.5 57.8 324 5 AAU85176 Aau85176 G-coupled
99 937.5 57.8 324 7 ADC86379 Adc86379 Human GPC
100 937.5 57.8 324 8 ADG83490 Adg83490 Human Olf

ALIGNMENTS

RESULT 1

AD109914
ID AD109914 standard; protein; 318 AA.

AC AD109914;

DT 22-APR-2004 (first entry)

DE Optimised 101P3A11v3 gene protein.

KW transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
KW stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.

OS Unidentified.

PN WO200292842-A2.

PD 21-NOV-2002.

PE 15-MAY-2002; 2002WO-US015520.

PR 15-MAY-2001; 2001US-0291118P.

PR 31-OCT-2001; 2001US-00001469.

PR 14-DEC-2001; 2001US-00017666.

XX (AGEN-) AGENSYS INC.

PI Jakobovits A, Farie M, Raitano AB, Morrison RK, Saffran D, Ge W,
PI Chaililta-Bid PM;

DR WPI; 2003-129310/12.

PT New composition comprising 101P3A11-related protein, useful for
PT preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
PT prostate, colon, kidney or breast cancer.

PS Claim 13; SEQ ID NO 5012; 327bp; English.

CC The invention relates to a novel composition comprising: a substance that
CC modulates the status of a protein comprising a sequence with a fully
CC defined 2466 or 3136 amino acid sequence given in the specification; or a
CC molecule that is immobilised by a protein comprising a sequence with a
CC fully defined 2466 or 3136 amino acids, where the status of a cell
CC expressing the protein is modulated. The invention further relates to: an
CC antibody; a non-human transgenic animal or hybridoma that produces the
CC antibody; a method of delivering a cytotoxic or diagnostic agent to a
CC cell that expresses the protein; a polynucleotide that encodes the
CC protein; a method for inhibiting the growth of cancer cells that express
CC the protein; a method for generating a mammalian immune response directed
CC to the protein; a method detecting in a sample the presence of a 101P3A11
CC -related protein or polynucleotide; and a method for monitoring one or
CC more 101P3A11 gene products in a biological sample from a patient having
CC or suspected of having cancer. The novel composition has cytostatic
CC activity. The composition is useful for preventing or treating cancer
CC e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
CC cancer. This sequence represents a 101P3A11 protein of the invention.

XX Sequence 318 AA;

Query Match 100.0%; Score 1622; DB 7; Length 318;

Best Local Similarity 100.0%; Pred. No. 1e-169;

Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGEBAQFWLAPFLCSLYLIVAGNLTTIIVRTSHLHE 60
|||||

DB 1 MMVDPNNGESSATYFIIIGLPGEBAQFWLAPFLCSLYLIVAGNLTTIIVRTSHLHE 60
QY PMYFLICMLSGIDILISTSSMPKMLAPWENSTTIOPACILQI PAHSLSGMESTVLLA 120
|||
DB 61 PMYFLICMLSGIDILISTSSMPKMLAPWENSTTIOPACILQI PAHSLSGMESTVLLA 120
|||
QY 121 MAPRYYAICHPLRHATVTLPRVTKIGVAAVVRGAALMAELPVFIKQLPFCRSNIISSH 180
DB 121 MAPRYYAICHPLRHATVTLPRVTKIGVAAVVRGAALMAELPVFIKQLPFCRSNIISSH 180
QY 181 YCHADYWKLA CDDIRNVVYGLVVISALIGDSLISFSYLLILKTVLGTTRBAQAAF 240
DB 181 YCHADYWKLA CDDIRNVVYGLVVISALIGDSLISFSYLLILKTVLGTTRBAQAAF 240
QY 241 GTCVSHVCAVPIFYVPFGLSMVRFKSRDSPPLVILANITLLVPPVLANPIYGVKTKE 300
DB 241 GTCVSHVCAVPIFYVPFGLSMVRFKSRDSPPLVILANITLLVPPVLANPIYGVKTKE 300
QY 301 IRORIILRFHVATHASBP 318
DB 301 IRORIILRFHVATHASBP 318

RESULT 2

AD109880
ID AD109880 standard; protein; 318 AA.

AC AD109880;

DT 22-APR-2004 (first entry)

DE 101P3A11v1 gene protein.

KW transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
KW stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.

OS Unidentified.

PN WO200292842-A2.

PD 21-NOV-2002.

PE 15-MAY-2002; 2002WO-US015520.

PR 15-MAY-2001; 2001US-0291118P.

PR 31-OCT-2001; 2001US-00001469.

PR 14-DEC-2001; 2001US-00017666.

XX (AGEN-) AGENSYS INC.

PI Jakobovits A, Farie M, Raitano AB, Morrison RK, Saffran D, Ge W,
PI Chaililta-Bid PM;

DR WPI; 2003-129310/12.

PT New composition comprising 101P3A11-related protein, useful for
PT preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
PT prostate, colon, kidney or breast cancer.

PS Claim 13; SEQ ID NO 4096; 327bp; English.

CC The invention relates to a novel composition comprising: a substance that
CC modulates the status of a protein comprising a sequence with a fully
CC defined 2466 or 3136 amino acid sequence given in the specification; or a
CC molecule that is immobilised by a protein comprising a sequence with a
CC fully defined 2466 or 3136 amino acids, where the status of a cell
CC expressing the protein is modulated. The invention further relates to: an
CC antibody; a non-human transgenic animal or hybridoma that produces the
CC antibody; a method of delivering a cytotoxic or diagnostic agent to a
CC cell that expresses the protein; a polynucleotide that encodes the
CC protein; a method for inhibiting the growth of cancer cells that express
CC the protein; a method for generating a mammalian immune response directed
CC to the protein; a method detecting in a sample the presence of a 101P3A11

CC -related protein or polynucleotide; and a method for monitoring one or
CC more 101P3A11 gene products in a biological sample from a patient having
CC or suspected of having cancer. The novel composition has cytostatic
CC activity. The composition is useful for preventing or treating cancer
CC e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
CC cancer. This sequence represents a 101P3A11 protein of the invention.
XX
SQ Sequence 318 AA;
Query Match 100.0%; Score 1622; DB 7; Length 318;
Best Local Similarity 100.0%; Pred. No. 1e-169;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVDPNGBSSATYFIIIGLPGLEBAQFWLAPLCSYLAVAGNTIIYVTEHSLHE 60
DB 1 MMVDPNGBSSATYFIIIGLPGLEBAQFWLAPLCSYLAVAGNTIIYVTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSMPPKMLAFWNSITTIOPDACLQIPAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSMPPKMLAFWNSITTIOPDACLQIPAIHSLSGMESTVLLA 120
QY 121 MAFDRYVALCHPLRHATVTLTPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHS 180
DB 121 MAFDRYVALCHPLRHATVTLTPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHS 180
QY 181 YCLHODVMKACDDIRVNVVYGLIIVIIISAIGLDSLISFSYLLILKTVLGLTREBAQKAF 240
DB 181 YCLHODVMKACDDIRVNVVYGLIIVIIISAIGLDSLISFSYLLILKTVLGLTREBAQKAF 240
QY 241 GTCVSHVCAVFIYVPFIIGLSMVHRFSKRDSPLPVILANIYLLVPPVLPPIYGVYKTK 300
DB 241 GTCVSHVCAVFIYVPFIIGLSMVHRFSKRDSPLPVILANIYLLVPPVLPPIYGVYKTK 300
QY 301 IRRRIILRLFRVATHASEP 318
DB 301 IRRRIILRLFRVATHASEP 318
RESULT 3
ADI09871
ID ADI09871 standard; protein; 318 AA.
XX
AC ADI09871;
XX
DT 22-APR-2004 (first entry)
XX
DB 101P3A11 protein region, amino acids 1-318.
XX
KM transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
XX stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.
XX
OS Unidentified.
XX
PN WO200292842-A2.
XX
PD 21-NOV-2002.
XX
PE 15-MAY-2002; 2002MO-US015520.
XX
PR 15-MAY-2001; 2001US-0291118P.
XX 31-OCT-2001; 2001US-00001469.
XX 14-DEC-2001; 2001US-00017666.
XX
XX (AGEN-) AGENSYS INC.
XX PA Jakobovits A, Paris M, Raitano AB, Morrison RK, Saffran D, Ge W;
XX PI Chailite-Eld PM;
XX WPI, 2003-129310/12.
XX
XX New composition comprising 101P3A11-related protein, useful for
XX preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
XX prostate, colon, kidney or breast cancer.

XX
PS Claim 13; SEQ ID NO 4087; 327bp; English.
XX
XX The invention relates to a novel composition comprising: a substance that
CC modulates the status of a protein comprising a sequence with a fully
CC defined 2466 or 3136 amino acid sequence given in the specification; or a
CC molecule that is immobilised by a protein comprising a sequence with a
CC fully defined 2466 or 3136 amino acids, where the status of a cell
CC expressing the protein is modulated. The invention further relates to: an
CC antibody; a non-human transgenic animal or hybridoma that produces the
CC antibody; a method of delivering a cytotoxic or diagnostic agent to a
CC cell that expresses the protein; a polynucleotide that encodes the
CC protein; a method for inhibiting the growth of cancer cells that express
CC the protein; a method for generating a mammalian immune response directed
CC to the protein; a method detecting in a sample the presence of a 101P3A11
CC -related protein or polynucleotide; and a method for monitoring one or
CC more 101P3A11 gene products in a biological sample from a patient having
CC or suspected of having cancer. The novel composition has cytostatic
CC activity. The composition is useful for preventing or treating cancer
CC e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
CC cancer. This sequence represents a protein region of the 101P3A11 protein
XX
SQ Sequence 318 AA;
Query Match 100.0%; Score 1622; DB 7; Length 318;
Best Local Similarity 100.0%; Pred. No. 1e-169;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVDPNGBSSATYFIIIGLPGLEBAQFWLAPLCSYLAVAGNTIIYVTEHSLHE 60
DB 1 MMVDPNGBSSATYFIIIGLPGLEBAQFWLAPLCSYLAVAGNTIIYVTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSMPPKMLAFWNSITTIOPDACLQIPAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSMPPKMLAFWNSITTIOPDACLQIPAIHSLSGMESTVLLA 120
QY 121 MAFDRYVALCHPLRHATVTLTPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHS 180
DB 121 MAFDRYVALCHPLRHATVTLTPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHS 180
QY 181 YCLHODVMKACDDIRVNVVYGLIIVIIISAIGLDSLISFSYLLILKTVLGLTREBAQKAF 240
DB 181 YCLHODVMKACDDIRVNVVYGLIIVIIISAIGLDSLISFSYLLILKTVLGLTREBAQKAF 240
QY 241 GTCVSHVCAVFIYVPFIIGLSMVHRFSKRDSPLPVILANIYLLVPPVLPPIYGVYKTK 300
DB 241 GTCVSHVCAVFIYVPFIIGLSMVHRFSKRDSPLPVILANIYLLVPPVLPPIYGVYKTK 300
QY 301 IRRRIILRLFRVATHASEP 318
DB 301 IRRRIILRLFRVATHASEP 318
RESULT 4
ADI09912
ID ADI09912 standard; protein; 338 AA.
XX
AC ADI09912;
XX
DT 22-APR-2004 (first entry)
XX
DB Optimised 101P3A11v1 gene protein.
XX
KM transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
XX stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.
XX
OS Unidentified.
XX
PN WO200292842-A2.
XX
PD 21-NOV-2002.

PF 15-MAY-2002; 2002MO-US015520.
XX
PR 15-MAY-2001; 2001US-0291118P.
PR 31-OCT-2001; 2001US-00001469.
PR 14-DEC-2001; 2001US-00017666.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Faris M, Raitano AB, Morrison RK, Saffran D, Ge W;
PI Chailita-Bid PM;
XX
DR WPI; 2003-129310/12.
XX
PT New composition comprising 101P3A11-related protein, useful for
PT preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
PT prostate, colon, kidney or breast cancer.
XX
PS Claim 13; SEQ ID NO 5010; 327PP; English.
XX
CC The invention relates to a novel composition comprising: a substance that
CC modulates the status of a protein comprising a sequence with a fully
CC defined 2466 or 3136 amino acid sequence given in the specification; or a
CC molecule that is immobilized by a protein comprising a sequence with a
CC fully defined 2466 or 3136 amino acids, where the status of a cell
CC expressing the protein is modulated. The invention further relates to: an
CC antibody; a non-human transgenic animal or hybridoma that produces the
CC antibody; a method of delivering a cytotoxic or diagnostic agent to a
CC cell that expresses the protein; a polynucleotide that encodes the
CC protein; a method for inhibiting the growth of cancer cells that express
CC the protein; a method for generating a mammalian immune response directed
CC to the protein; a method detecting in a sample the presence of a 101P3A11
CC -related protein or polynucleotide; and a method for monitoring one or
CC more 101P3A11 gene products in a biological sample from a patient having
CC or suspected of having cancer. The novel composition has cytostatic
CC activity. The composition is useful for preventing or treating cancer
CC e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
CC cancer. This sequence represents a 101P3A11 protein of the invention.
XX
SQ Sequence 338 AA:

Query Match 100.0%; Score 1622; DB 7; Length 338;
Best Local Similarity 100.0%; Pred. No. 1,1e-169;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNBSATPFIILGLPGLERQFWLAPLCSLYLIVLGNLTIIYVTRHSLSH 60
DB 1 MMVDPNGNBSATPFIILGLPGLERQFWLAPLCSLYLIVLGNLTIIYVTRHSLSH 60
QY 61 PMYIFLCMLSGIDILISTSNPKMLAIFWNSTTIQPDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSNPKMLAIFWNSTTIQPDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAPRVAIACPLRAATVLTIPRTKIGVAAVVGAAALMELPFIKQLPFCRSNLSHS 180
DB 121 MAPRVAIACPLRAATVLTIPRTKIGVAAVVGAAALMELPFIKQLPFCRSNLSHS 180
QY 121 MAPRVAIACPLRAATVLTIPRTKIGVAAVVGAAALMELPFIKQLPFCRSNLSHS 180
DB 121 MAPRVAIACPLRAATVLTIPRTKIGVAAVVGAAALMELPFIKQLPFCRSNLSHS 180
QY 181 YCLHODVWKLACDDIRVNVVGLVYISAGIDSLISFSYLLIKTYLGLTRBAQAKAF 240
DB 181 YCLHODVWKLACDDIRVNVVGLVYISAGIDSLISFSYLLIKTYLGLTRBAQAKAF 240
QY 241 GTCVSHVCAVEIPVYPIGLSMVHRFSKRRDSPLEVIANTLYLVPPVLANPIVGVKTK 300
DB 241 GTCVSHVCAVEIPVYPIGLSMVHRFSKRRDSPLEVIANTLYLVPPVLANPIVGVKTK 300
QY 301 IRORILRLFHVATASEP 318
DB 301 IRORILRLFHVATASEP 318
XX
RESULT 5
AAIY92365
ID AAY92365 standard; protein; 318 AA.

AC AAY92365;
XX
DT 10-AUG-2000 (first entry)
XX
DE G protein-coupled receptor protein 5.
XX
KW GPCR-5; G protein-coupled receptor protein; antipsoriatic; antirheumatic;
KW immunosuppressive; antitumor; antineoplastic; antineoplastic;
KW antithyroid; cytostatic; hepatotropic; dermatological; anti-inflammatory;
KW antigout; thyromimetic; hemostatic; virucide; hepatotropic; osteopathic;
KW antiparasitic; immunostimulant.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide
FT Modified-site
FT 8
FT /note= "potential glycosylation site"
FT /label= signal_peptide
FT 1..26
FT /label= "potential glycosylation site"
FT 34..52
FT /label= transmembrane
FT Modified-site
FT 45
FT /note= "potential glycosylation site"
FT 57
FT /note= "potential phosphorylation site"
FT 62..83
FT /label= signature_sequence
FT /note= "G-protein-coupled receptor"
FT 70
FT /note= "potential phosphorylation site"
FT 91
FT /note= "potential glycosylation site"
FT Modified-site
FT 111
FT /note= "potential phosphorylation site"
FT 113..129
FT /label= signature_sequence
FT /note= "G-protein coupled receptor"
FT 180..194
FT /label= signature_sequence
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FT 240..255
FT /label= signature_sequence
FT /note= "G-protein coupled receptor"
FT 267
FT /note= "potential phosphorylation site"
FT 272
FT /note= "potential phosphorylation site"
XX
PN WO200020590-A2.
XX
PD 13-APR-2000.
XX
XX 06-OCT-1999; 99WD-US023317.
XX
XX 06-OCT-1998; 98US-00167219.
XX 06-OCT-1998; 98US-0172211P.
PR 11-MAY-1999; 99US-0133585P.
XX
XX (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lal P, Bandman O, Au-Young J, Reddy R;
PI Corley NC, Guegler KJ, Gorgone GA, Baughn MR, Azimzal Y;
XX WPI; 2000-328934/28.
XX N-PSDB; AAA09351.
XX
PT Novel human G-protein coupled receptor proteins used in the diagnosis,
PT treatment and prevention of nervous system disorders,
PT autoimmune/inflammatory disorders, and cell proliferative disorders such
PT as cancer.
XX

PS Claim 1; Page 71-72; 84pp; English.

CC This sequence encodes human G-protein coupled receptor protein (GCRP) 5.

CC The GCRP polypeptides, polynucleotides, antibodies, antagonists and

CC agonists may be administered to human patients for the diagnosis,

CC treatment and prevention of nervous system disorders (e.g. epilepsy,

CC stroke, neoplasms, Alzheimer's disease), autoimmune or inflammatory

CC disorders, complications of cancer, hemodialysis and extracorporeal

CC circulation, and cell proliferative disorders. They are also used to

CC treat or prevent disorders associated with decreased or increased

CC expression or activity of GCRP

XX

XX Sequence 318 AA:

Query Match 99.8%; Score 1619; DB 3; Length 318;

Best Local Similarity 99.7%; Pred. No. 2.2e-169;

Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLAVGNLTITIVYRTESLHE 60

DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLAVGNLTITIVYRTESLHE 60

QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120

DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120

QY 121 MAFPRYVAICPLRHAATVLTLPRTYKIGVAAVVGALMALPVPFIQOLPFCRSNIISHS 180

DB 121 MAFPRYVAICPLRHAATVLTLPRTYKIGVAAVVGALMALPVPFIQOLPFCRSNIISHS 180

QY 181 YCLHQDVWKLACDDIRNVVYGLVITISAIGLDLSLISFSYLLTKTVLGLTREAOAKAF 240

DB 181 YCLHQDVWKLACDDIRNVVYGLVITISAIGLDLSLISFSYLLTKTVLGLTREAOAKAF 240

QY 241 GTCVSHVCAVFIYPVPFIGLSMVHRFSKRSDSPVLILANITYLLVPPVLPVIYGVYKKE 300

DB 241 GTCVSHVCAVFIYPVPFIGLSMVHRFSKRSDSPVLILANITYLLVPPVLPVIYGVYKKE 300

QY 301 IRQRILRLFHVAATHASEP 318

DB 301 IRQRILRLFHVAATHASEP 318

RESULT 6

AA001306

ID AA001306 standard; protein; 318 AA.

AC AA001306;

XX

XX 04-OCT-2001 (first entry)

XX

XX P835P amino acid sequence.

XX

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;

XX cytostatic; gene therapy; metastasis.

XX

XX Homo sapiens.

XX

XX WO200151633-A2.

XX

XX 19-JUL-2001.

XX

XX 16-JAN-2001; 2001WO-US001574.

XX

XX 14-JAN-2000; 2000US-00483672.

XX

XX (CORI-) CORIXA CORP.

XX

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,

XX PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelty YAM,

XX PI Wang A, Meagher MJ;

XX

XX WPI; 2001-425873/45.

XX

PT New polynucleotide encoding a prostate-specific protein, for diagnosing,

PT monitoring and treating prostate cancer in a patient and for use in

PT vaccines.

XX

XX Claim 2; Page 534-535; 543pp; English.

CC The present invention describes polynucleotide sequences (I) which encode

CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,

CC and can be used in vaccine production and gene therapy. (I), (II),

CC antibodies to (II), fusion proteins comprising (II), and isolated T cells

CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and

CC the antibodies are also used in the detection of cancer in a patient. The

CC cancer that is diagnosed or treated is particularly prostate cancer. (I)

CC and (II) can be used in vaccines. The antibodies or (I) can be used for

CC monitoring the progression of cancer in a patient. (I) and (II) can also

CC be used to improve diagnostic and therapeutic methods for prostate

CC cancer. They can indicate the level of metastasis as well as the prostate

CC volume. AAH93357 to AAH93944 and AA001115 to AA001318 represent

CC polynucleotide and amino acid sequences used in the exemplification of

CC the present invention

XX

XX Sequence 318 AA:

Query Match 99.8%; Score 1619; DB 4; Length 318;

Best Local Similarity 99.7%; Pred. No. 2.2e-169;

Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLAVGNLTITIVYRTESLHE 60

DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLAVGNLTITIVYRTESLHE 60

QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120

DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120

QY 121 MAFPRYVAICPLRHAATVLTLPRTYKIGVAAVVGALMALPVPFIQOLPFCRSNIISHS 180

DB 121 MAFPRYVAICPLRHAATVLTLPRTYKIGVAAVVGALMALPVPFIQOLPFCRSNIISHS 180

QY 181 YCLHQDVWKLACDDIRNVVYGLVITISAIGLDLSLISFSYLLTKTVLGLTREAOAKAF 240

DB 181 YCLHQDVWKLACDDIRNVVYGLVITISAIGLDLSLISFSYLLTKTVLGLTREAOAKAF 240

QY 241 GTCVSHVCAVFIYPVPFIGLSMVHRFSKRSDSPVLILANITYLLVPPVLPVIYGVYKKE 300

DB 241 GTCVSHVCAVFIYPVPFIGLSMVHRFSKRSDSPVLILANITYLLVPPVLPVIYGVYKKE 300

QY 301 IRQRILRLFHVAATHASEP 318

DB 301 IRQRILRLFHVAATHASEP 318

RESULT 7

AA069951

ID AA069951 standard; protein; 318 AA.

AC AA069951;

XX

XX 30-JAN-2002 (first entry)

XX

XX Human prostate cDNA encoded protein #85.

XX

XX Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.

XX

XX Homo sapiens.

XX

XX WO200173032-A2.

XX

XX 04-OCT-2001.

XX

XX 27-MAR-2001; 2001WO-US009919.

27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
DR N-PSDB; AAS64174, AAS64176, AAS64177.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
XX
PS Claim 2; Page 568-569; 579pp; English.
XX
CC The invention relates to isolated prostate-specific polynucleotides,
CC polypeptides, fusion proteins of the polypeptides, antibodies raised
CC against the polypeptides (or antigenic epitopes derived from them) and
CC antigen-presenting cells expressing the polypeptides. The antibodies are
CC useful for detecting the presence of cancer, especially prostate cancer.
CC The polypeptides, polynucleotides and the antigen-presenting cells are
CC useful for stimulating and/or expanding T cells specific for a tumor
CC protein, and for inhibiting the development of cancer especially prostate
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC useful for stimulating an immune response, and for treating cancer. The
CC oligonucleotide is useful for detecting cancer. The present sequence is a
CC prostate specific polypeptide of the invention
XX
SQ Sequence 318 AA;
Query Match 99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 2.2e-169;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVDPNNGESSATYFIILGLPGLBAQFWLAPFLCSLYLNAVGNLTITTYIVRTEHSLHE 60
DB 1 MMVDPNNGESSATYFIILGLPGLBAQFWLAPFLCSLYLNAVGNLTITTYIVRTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQDPACLLQIPALHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQDPACLLQIPALHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIISHS 180
QY 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIISHS 180
QY 181 YCLHQDVWKLACDDIRVVVYGLIIVISAIGDSLISFSYLLIKTLYLGLTREAOAKAF 240
DB 181 YCLHQDVWKLACDDIRVVVYGLIIVISAIGDSLISFSYLLIKTLYLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDPLPVILANTYLLVPVLANPIVGVKTXE 300
DB 241 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDPLPVILANTYLLVPVLANPIVGVKTXE 300
QY 301 IRRIRILRLFHVATHASEP 318
DB 301 IRRIRILRLFHVATHASEP 318
RESULT 8
AAG71659
ID AAG71659 standard; protein; 318 AA.

XX
AC AAG71659;
XX
DT 30-JUN-2001 (first entry)
XX
DS Human olfactory receptor polypeptide, SEQ ID NO: 1340.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027582.
XX
PR 08-OCT-1999; 99US-0158615P.
PR 24-FEB-2000; 2000US-0184809P.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
XX
PS Claim 11; Page 826-827; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by one of
CC a number of novel polynucleotides. The polynucleotides can be used in
CC screening for olfactory agonists and antagonists. The methods allow for
CC the determination of primary scents and the identification of the odour
CC receptors used to detect these primary scents. The methods also enable
CC determination of secondary scents and the identification of combinations
CC of odour receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called a
CC scent fingerprint or scent profile), which may be used to re-create and
CC edit scents. Libraries of olfactory receptors are useful for determining
CC the interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
CC individuals
XX
SQ Sequence 318 AA;
Query Match 99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 2.2e-169;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVDPNNGESSATYFIILGLPGLBAQFWLAPFLCSLYLNAVGNLTITTYIVRTEHSLHE 60
DB 1 MMVDPNNGESSATYFIILGLPGLBAQFWLAPFLCSLYLNAVGNLTITTYIVRTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQDPACLLQIPALHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQDPACLLQIPALHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIISHS 180
QY 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIISHS 180
QY 181 YCLHQDVWKLACDDIRVVVYGLIIVISAIGDSLISFSYLLIKTLYLGLTREAOAKAF 240
DB 181 YCLHQDVWKLACDDIRVVVYGLIIVISAIGDSLISFSYLLIKTLYLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDPLPVILANTYLLVPVLANPIVGVKTXE 300
DB 241 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDPLPVILANTYLLVPVLANPIVGVKTXE 300

KM anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity;
 KM anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
 KM achina; Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KM infection; human immunodeficiency virus; HIV.
 OS Homo sapiens.
 XX
 PN WO200174904-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US010241.
 XX
 PR 05-MAR-2000; 2000US-0193664P.
 PR 05-APR-2000; 2000US-0194614P.
 PR 06-APR-2000; 2000US-0195063P.
 PR 06-APR-2000; 2000US-0195066P.
 PR 06-APR-2000; 2000US-0195067P.
 PR 06-APR-2000; 2000US-0195068P.
 PR 06-APR-2000; 2000US-0195069P.
 PR 06-APR-2000; 2000US-0195070P.
 PR 06-APR-2000; 2000US-0195510P.
 PR 21-JUL-2000; 2000US-0219855P.
 PR 27-JUL-2000; 2000US-0221284P.
 PR 28-JUL-2000; 2000US-0221325P.
 PR 11-AUG-2000; 2000US-0234588P.
 PR 11-OCT-2000; 2000US-0239613P.
 PR 18-JAN-2001; 2001US-0262508P.
 PR 23-JAN-2001; 2001US-0263433P.
 PR 23-JAN-2001; 2001US-0263604P.
 PR 30-JAN-2001; 2001US-0265161P.
 PR 29-MAR-2001; 2001US-00823172.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Majumder K, Vernet CM, Casman SJ, Wolenc AR, Spaderna SK;
 PI Padigaru M, Mishra VS, Tchervet VT, Spytek KA, Li L, Baumgartner JC;
 PI Gusev VY;
 XX
 DR WPI, 2001-639351/73.
 XX N-PSDB; ABA81542.
 XX
 PT New human G-protein coupled receptor X, GPCR, polypeptide useful in
 PT treatment or prevention of GPCR associated disorders e.g. cardiomyopathy
 PT or atherosclerosis, and to screen for antagonists and agonists useful
 PT therapeutically.
 XX
 PS Claim 1; Page 55; 157pp; English.
 XX
 CC The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
 CC encode G-coupled protein-receptor related polypeptides (ABA84522-
 CC ABA84543). The isolated polypeptide having a sequence differing by no
 CC more than 15 % of amino acid residues from one of 22 amino acid sequences
 CC (or mature forms of the sequences), fully defined in the specification
 CC and corresponding to human G-protein coupled receptor X (GPCRX)
 CC polypeptides. The polypeptides have potential cardiac,
 CC antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The
 CC polypeptides can be administered therapeutically, especially using gene
 CC therapy and expressing the encoding DNA in vivo, to treat or prevent
 CC GPCR-associated disorders, especially in humans. For example, they can
 CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
 CC related to signal processing and metabolic pathway modulation (e.g. obesity,
 CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
 CC sclerosis, asthma, cancer, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease), immune disorders,
 CC hematopoietic disorders, developmental diseases, neurological disorders,
 CC bacterial, fungal, protozoal and viral infections (e.g. with human
 CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
 CC to determine the presence of or predisposition to a disease associated
 CC with altered levels of the polypeptide in mammals (especially humans) by
 CC detecting alterations in polypeptide expression levels relative to
 CC control samples. They are useful to identify agents binding polypeptide
 CC (e.g. cellular receptors or downstream effectors) and/or agents

CC modulating cellular polypeptide expression or activity, useful as
 CC antagonists and agonists in disease treatment
 XX
 SO Sequence 318 AA;
 Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. NO. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVDPNNGESSATYFTLLIGLGLBEAQFWLAPLCSLYLAVGNLTIIYIVRSHLSHE 60
 DB 1 MMVDPNNGESSATYFTLLIGLGLBEAQFWLAPLCSLYLAVGNLTIIYIVRSHLSHE 60
 QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWFNSTTIQFDACILQIFAIHLSGMESTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWFNSTTIQFDACILQIFAIHLSGMESTVLLA 120
 QY 121 MAPDRYVAICHPLRHATVTLTPVTXIGVAAVYRGAAALMAPLPVFIKQLPCCRNIISHS 180
 DB 121 MAPDRYVAICHPLRHATVTLTPVTXIGVAAVYRGAAALMAPLPVFIKQLPCCRNIISHS 180
 QY 121 MAPDRYVAICHPLRHATVTLTPVTXIGVAAVYRGAAALMAPLPVFIKQLPCCRNIISHS 180
 DB 121 MAPDRYVAICHPLRHATVTLTPVTXIGVAAVYRGAAALMAPLPVFIKQLPCCRNIISHS 180
 QY 181 YCLHODYMKIACDDIRNNVYGLIIVISATIGLDSLISFSLVILIKTVLGLTREAOAKAF 240
 DB 181 YCLHODYMKIACDDIRNNVYGLIIVISATIGLDSLISFSLVILIKTVLGLTREAOAKAF 240
 QY 241 GTCVSHVCAVFIFFVPEIGLSMYRFSKRDSPLPVILANIYLLVPPVLPVYGVATKES 300
 DB 241 GTCVSHVCAVFIFFVPEIGLSMYRFSKRDSPLPVILANIYLLVPPVLPVYGVATKES 300
 QY 301 IRRRIIRLPHVATHASRP 318
 DB 301 IRRRIIRLPHVATHASRP 318
 RESULT 11
 AB071842
 ID AB071842 standard; protein; 318 AA.
 XX
 AC AB071842;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Prostate cancer associated protein #66.
 XX
 KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PSMA.
 XX
 OS Homo sapiens.
 XX
 XX US2002192763-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 29-JUN-2001; 2001US-00895793.
 XX
 PR 04-OCT-1999; 99US-0157455P.
 PR 04-OCT-2000; 2000US-00679272.
 PR 28-MAR-2001; 2001US-00822827.
 XX
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.

QY 241 GTCVSHCAVFIFVVPFGLSMVHRSKRDSPVLILANITYLLVPPVLANPIYGVGVTKE 300
DB 241 GTCVSHCAVFIFVVPFGLSMVHRSKRDSPVLILANITYLLVPPVLANPIYGVGVTKE 300
QY 301 IRRRIILRFHVATASEP 318
DB 301 IRRRIILRFHVATASEP 318
RESULT 13
ABP95411
ID ABB95411 standard; protein, 318 AA.
AC ABB95411;
XX 19-JUL-2002 (first entry)
XX Human P835P protein SEQ ID NO 920.
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy.
XX Homo sapiens.
XX OS
XX US2002022248-A1.
XX PD 21-FEB-2002.
XX PF 12-JAN-2001; 2001US-00759143.
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 18-NOV-1999; 99US-00439313.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX WPI: 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX Claim 2; SEQ ID NO 920; 87bp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a
CC protein described in the invention
XX
XX Sequence 318 AA;
SQ
Query Match 99.8%; Score 1619; DB 5; Length 318;
Best Local Similarity 99.7%; Pred. No. 2.2e-169;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWDVDPNGNESSATYFIILGPGLEAOFWLAFLCSYLLAVLGNLTITTYVREHSLHE 60
DB 1 MWDVDPNGNESSATYFIILGPGLEAOFWLAFLCSYLLAVLGNLTITTYVREHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKWLAFWFNSTTIOPDACLQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKWLAFWFNSTTIOPDACLQIFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHATVLTLPRTKIGVAAVVGAAIMAPLPVFIKOLPECRSNILSHS 180
DB 121 MAFDRYVAICHPLRHATVLTLPRTKIGVAAVVGAAIMAPLPVFIKOLPECRSNILSHS 180
QY 181 YCHQDVMKACDRIKRVNVTYGLIIVISAIGLDSLLISFSTYLLIKTVLGLTRBAQAKAF 240
DB 181 YCHQDVMKACDRIKRVNVTYGLIIVISAIGLDSLLISFSTYLLIKTVLGLTRBAQAKAF 240
QY 241 GTCVSHCAVFIFVVPFGLSMVHRSKRDSPVLILANITYLLVPPVLANPIYGVGVTKE 300
DB 241 GTCVSHCAVFIFVVPFGLSMVHRSKRDSPVLILANITYLLVPPVLANPIYGVGVTKE 300
QY 301 IRRRIILRFHVATASEP 318
DB 301 IRRRIILRFHVATASEP 318
RESULT 14
ABP95674
ID ABB95674 standard; protein, 318 AA.
XX
XX ABB95674;
XX 06-MAR-2003 (first entry)
XX
XX Human GPCR polypeptide SEQ ID NO 158.
XX
XX Human GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; receptor.
XX
XX Homo sapiens.
XX OS
XX WO200216548-A2.
XX PN 28-FEB-2002.
XX PD 30-JUL-2001; 2001WO-IB001446.
XX PF 04-AUG-2000; 2000JP-00237818.
XX PR 13-FEB-2001; 2001JP-00034434.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Haga T, Takeda S, Mitaku S;
 XX WPI; 2002-304118/34.
 DR N-PSDB; AB242948.
 XX Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 XX Claim 10; SEQ ID NO 158; 97pp + Sequence listing; Japanese.
 XX
 CC The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-
 CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets
 CC for drug development e.g. based on olfactory and gustatory receptors in
 CC form of agonists and antagonists by screening intrinsic and extrinsic
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 318 AA;
 Query Match 99.8%; Score 1619; DB 5; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFMFLAPLCSLYLAVANGNTIIYIVRTESLHE 60
 DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFMFLAPLCSLYLAVANGNTIIYIVRTESLHE 60
 QY 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIQFDACILQIFAHISLGSMESTVLLA 120
 DB 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIQFDACILQIFAHISLGSMESTVLLA 120
 QY 121 MADDRVYALCHPRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHS 180
 DB 121 MADDRVYALCHPRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHS 180
 QY 181 YCHLQDVAKLACDDIRNVVYGLIIVISAIGLSLISFSYLLILKTVLGLTRBAQKAF 240
 DB 181 YCHLQDVAKLACDDIRNVVYGLIIVISAIGLSLISFSYLLILKTVLGLTRBAQKAF 240
 QY 241 GTCVSHCAVFIFFVPIGISMVHRFSKRDSPLPVILANIYLLVPPVLPVIYGVGTKS 300
 DB 241 GTCVSHCAVFIFFVPIGISMVHRFSKRDSPLPVILANIYLLVPPVLPVIYGVGTKS 300
 QY 301 IRRQRIILRFVATHTASEP 318
 DB 301 IRRQRIILRFVATHTASEP 318
 RESULT 15
 ID AAU95746 standard; protein; 318 AA.
 AC AAU95746;
 XX
 XX 02-JUL-2002 (first entry)
 XX Human olfactory and pheromone G protein-coupled receptor #233.
 XX
 KM Human; olfactory and pheromone G protein coupled; receptor; GPCR;
 KM transquillizer; antidepressant; neuroleptic; endocrine; anabolic;
 KM anorectic; taste; fragrance; food additive; cosmetic; cell migration;
 KM sterility; psychotic disorder; neurological disorder; anxiety;
 KM schizophrenia; manic depression; depression; axonal growth;
 KM menstrual cycle; appetite sexual motivation; sexual attraction;
 KM aggression.
 XX

OS Homo sapiens.
 XX
 XX W0200224726-A2.
 PN
 XX 28-MAR-2002.
 PD
 XX
 XX 21-SEP-2001; 2001WO-BE000162.
 PF
 XX 22-SEP-2000; 2000EP-00870211.
 PK
 XX (CHEM-) CHEMCOM SA.
 PA
 XX
 PI Velthen A;
 XX
 DR WPI; 2002-330013/36.
 DR N-PSDB; ABK68633.
 XX
 PT Novel pheromone G-protein coupled receptor and receptor-derived agonists,
 PT antagonists or inhibitors useful in food or cosmetic products or in the
 PT treatment or prevention of neurological disorders such as anxiety and
 PT schizophrenia.
 XX
 PS Disclosure; Page 710-711; 833pp; English.
 XX
 CC The invention relates to olfactory and Pheromone G-protein coupled
 CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
 CC portion and its encoding polynucleotide. Also included are an agonist,
 CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector
 CC comprising the polynucleotide, a cell transformed by the vector, a non-
 CC human mammal comprising a partial or total deletion of the polynucleotide
 CC encoding the receptor and screening (detection and possibly, recovering)
 CC of compounds which are known or not known to be agonist, antagonists or
 CC inhibitors of natural compounds to the GPCR. The receptor-derived
 CC agonists, antagonists, inhibitors or compounds are used as an
 CC improvement, elimination or substitution of an existing taste and/or a
 CC fragrance of (or in) the food and/or cosmetic products. They can also be
 CC used in the preparation of medicament in the treatment and/or prevention
 CC of a mammalian disorder, such as cell migration, sterility, psychotic and
 CC neurological disorders, including anxiety, schizophrenia, manic
 CC depression, depression, for promoting axonal growth, nerve cell
 CC connection and nerve regeneration for modulating male and female
 CC endocrine functions, hormone production and the menstrual cycle, for the
 CC prevention or the treatment by stimulation of several mammalian
 CC behaviours, such as stimulation or suppression of appetite, sexual
 CC motivation, sexual attraction, aggression and for promoting or
 CC suppressing chemical communication between organisms. The present
 CC sequence is a human olfactory and pheromone GPCR protein sequence
 CC
 SQ Sequence 318 AA;
 Query Match 99.8%; Score 1619; DB 5; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFMFLAPLCSLYLAVANGNTIIYIVRTESLHE 60
 DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFMFLAPLCSLYLAVANGNTIIYIVRTESLHE 60
 QY 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIQFDACILQIFAHISLGSMESTVLLA 120
 DB 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIQFDACILQIFAHISLGSMESTVLLA 120
 QY 121 MADDRVYALCHPRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHS 180
 DB 121 MADDRVYALCHPRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHS 180
 QY 181 YCHLQDVAKLACDDIRNVVYGLIIVISAIGLSLISFSYLLILKTVLGLTRBAQKAF 240
 DB 181 YCHLQDVAKLACDDIRNVVYGLIIVISAIGLSLISFSYLLILKTVLGLTRBAQKAF 240
 QY 241 GTCVSHCAVFIFFVPIGISMVHRFSKRDSPLPVILANIYLLVPPVLPVIYGVGTKS 300
 DB 241 GTCVSHCAVFIFFVPIGISMVHRFSKRDSPLPVILANIYLLVPPVLPVIYGVGTKS 300

QY 301 IRORIILRFHVATASEP 318
DB 301 IRORIILRFHVATASEP 318

RESULT 16
AAU85181
ID AAU85181 standard; protein; 318 AA.

AC AAU85181;
DT 08-MAY-2002 (first entry)
XX G-coupled olfactory receptor #42.
DE G-coupled olfactory receptor #42.
XX Human; olfactory G-coupled receptor; sensory perception of odourant;
KM odour composition; taste composition.
XX Homo sapiens.
OS
XX WO200198526-A2.
PN
XX 27-DEC-2001.
PD
XX 22-JUN-2001; 2001WO-US020122.
PF
XX 22-JUN-2000; 2000US-0213812P.
PR 13-MAR-2001; 2001US-00804291.
XX
XX (SENO-) SENOMYX INC.
PA
XX Zozulya S, Stryer L;
PI WPI; 2002-083330/11.
DR N-PSDB; ABK37540.
XX
XX Representing sensory perception of one or more odourants for the
PT identification and design of tastes and odors comprises providing a
PT representative group of n olfactory receptors.
XX
XX Claim 1; Page 77; 182pp; English.

CC The invention relates to a method of representing sensory perception of
CC one or more odourants. The method comprises: (a) providing a
CC representative class of n olfactory receptors or ligand binding domains
CC (LBD) of these receptors; (b) measuring values X1 to Xn representative of
CC at least one activity of one or more odourants selected from: (i) binding
CC one or more odourants to the LBD of at least one of the n olfactory
CC receptors; (ii) activating at least one of the n olfactory receptors with
CC the one or more odourants; and (iii) blocking at least one of the n
CC olfactory receptors with the one or more odourants; and (c) generating a
CC representation of sensory perception from the values X1 to Xn. The
CC representation of the sensory perception of odourants is useful for the
CC design and formulation of odour and taste compositions. AAU85140-AAU85393
CC represent human olfactory G-coupled receptor amino acid sequences of the
CC invention
XX
SQ Sequence 318 AA;

Query Match 99.8%; Score 1619; DB 5; Length 318;
Best Local Similarity 99.7%; Pred. No. 2.2e-169;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVDPNNGESSATFILIGLPGLEBAQFWLAPLCSLYLIANLNTIIYVTRHSHAE 60
DB 1 MMVDPNGNESSATFILIGLPGLEBAQFWLAPLCSLYLIANLNTIIYVTRHSHAE 60
QY 61 PMYFLCMLSGIDILISTSSMPKMLAIFWPNSTTIQDPACLLQTPAHSLSGMSTVLLA 120
DB 61 PMYFLCMLSGIDILISTSSMPKMLAIFWPNSTTIQDPACLLQTPAHSLSGMSTVLLA 120
QY 121 MAFDRYVAICHPLRHATVLTLPVTYKIGVAAVRGALMALMPVFIKQLPFCRSNLSHS 180

DB 121 MAFDRYVAICHPLRHATVLTLPVTYKIGVAAVRGALMALMPVFIKQLPFCRSNLSHS 180
QY 181 YCHADQPMKACCDIRNNVYGLIVITISATGDSLLISFETYLITKTVLGTTRAQAKAF 240
DB 181 YCHADQPMKACCDIRNNVYGLIVITISATGDSLLISFETYLITKTVLGTTRAQAKAF 240
QY 241 GTCVSHVCAVFIYPVPIGLSMYHRSKRSDSPPLVLIANIYLLVPPVLNPIVGVKTKS 300
DB 241 GTCVSHVCAVFIYPVPIGLSMYHRSKRSDSPPLVLIANIYLLVPPVLNPIVGVKTKS 300
QY 301 IRORIILRFHVATASEP 318
DB 301 IRORIILRFHVATASEP 318

RESULT 17
ABO19491
ID ABO19491 standard; protein; 318 AA.

AC ABO19491;
DT 28-AUG-2003 (first entry)
XX
XX Human G protein-coupled receptor HGPBMY4.
DE
XX Human; receptor; G protein-coupled receptor; HGPBMY4; prostatitis;
KM Chagas's disease; post-inflammatory pseudotumour; infection; asthma;
KM benign prostatic hyperplasia; cancer; anorexia; Parkinson's disease;
KM acute heart failure; hypotension; hypertension; osteoporosis; ulcer;
KM neurological disorder; AIDS; allergy; anaemia; atherosclerosis;
KM Crohn's disease; atopic dermatitis; diabetes mellitus; emphysema;
KM Grave's disease; lupus erythematosus; multiple sclerosis; vaccine;
KM myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis;
KM rheumatoid arthritis; psoriasis; Sjogren's syndrome; trauma;
KM autoimmune thyroiditis; Alzheimer's disease; amnesia; bipolar disorder;
KM amyotrophic lateral sclerosis; schizophrenia; Tourette's disorder.
XX
XX Homo sapiens.
OS
XX US2003022237-A1.
PN
XX 30-JAN-2003.
PD
XX 26-SEP-2001; 2001US-00966459.
PF
XX 27-SEP-2000; 2000US-0235833P.
PR 16-JAN-2001; 2001US-0261776P.
PR 13-JUN-2001; 2001US-0305351P.
PR 17-AUG-2001; 2001US-0313202P.
XX
XX (FEDER/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.
PA (CACACE/) CACACE A.
PA (BARBER/) BARBER L.
PA (KORN/) KORNACKER M G.
XX
XX Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace A;
PI Barber L, Kornacker MG;
XX WPI; 2003-492001/46.
DR N-PSDB; ACD29000.

XX New human G-protein coupled receptor polypeptide, HGPBMY4, expressed
XX highly in prostate, colon and lung, useful for treating, preventing
XX cancer, immune, neurological, cardiovascular, colon and lung-related
XX disorders.
XX Claim 11; Fig 2; 74pp; English.
XX The invention relates to a new isolated G protein-coupled receptor

CC polypeptide HGPBMY4, comprising a sequence at least 95% identical to the
 CC protein appearing as ABO13491, or the encoded sequence of ATCC PTA-2682,
 CC the polypeptide fragment, domain, epitope, allelic variant, species
 CC homologue or a polypeptide corresponding to amino acids 2-318 of
 CC HGPBMY4. Also included are the nucleic acid encoding HGPBMY4 (and its
 CC fragment, allelic variant and complements), a recombinant vector
 CC comprising the nucleic acid, a recombinant host cell comprising the
 CC nucleic acid (and expressing HGPBMY4), an anti-HGPBMY4 antibody, a gene
 CC corresponding to the HGPBMY4 cDNA sequence, a compound that modulates
 CC the biological activity of human HGPBMY4, a cell comprising NFAT/CRE
 CC (not defined) and HGPBMY4 and a cell comprising NFAT G alpha 15 and
 CC HGPBMY4. HGPBMY4 or nucleic acid is useful for preventing, treating, or
 CC ameliorating e.g. a disease, disorder, or condition related to colon,
 CC breast, ovaries, or immune system (e.g. prostatitis, Chagas's disease,
 CC post-inflammatory pseudotumour, benign prostatic hyperplasia, bacterial,
 CC fungal, protozoan, and viral infections, particularly HIV-1 and HIV-2,
 CC cancers, anorexia, asthma, Parkinson's disease, acute heart failure,
 CC hypertension, hyperextension, urinary retention, osteoporosis, ulcers,
 CC neurological disorders, AIDS, Addison's disease, allergies, anaemia,
 CC atherosclerosis, bronchitis, Crohn's disease, ulcerative colitis, atopic
 CC dermatitis, diabetes mellitus, emphysema, glomerulonephritis, gout,
 CC Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia
 CC gravis, myocardial or pericardial inflammation, osteoarthritis,
 CC osteoporosis, pancreatitis, rheumatoid arthritis, psoriasis, scleroderma,
 CC Sjogren's syndrome, and autoimmune thyroiditis, complications of cancer,
 CC haemodialysis and extracorporeal circulation, trauma, Alzheimer's
 CC disease, amnesia, amyotrophic lateral sclerosis, bipolar disorder,
 CC schizophrenia, and Tourette's disorder. HGPBMY4 is also useful as a
 CC vaccine. HGPBMY4 is useful for identifying binding partners and
 CC ant/agonists. The present sequence represents HGPBMY4

XX Sequence 318 AA:

Query Match 99.8%; Score 1619; DB 6; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPCSLYLAVGNLTIIYVREHSLH 60
 DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPCSLYLAVGNLTIIYVREHSLH 60
 QY 61 PMYIFLCMSGIDILISTSMRPMKLAIFWNSSTTIQPDACLQIFAIHSLSGMESTVLLA 120
 DB 61 PMYIFLCMSGIDILISTSMRPMKLAIFWNSSTTIQPDACLQIFAIHSLSGMESTVLLA 120
 QY 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVGALMAMPVPFIKQLPFCRSNIIISHS 180
 DB 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVGALMAMPVPFIKQLPFCRSNIIISHS 180
 QY 181 YCLHODVMKLAACDRIKVVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 DB 181 YCLHODVMKLAACDRIKVVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIIVPPIGISMVHRFSKRDSPLPVLIANIYLLVPPVLPVIYGVYTKS 300
 DB 241 GTCVSHCAVFIIVPPIGISMVHRFSKRDSPLPVLIANIYLLVPPVLPVIYGVYTKS 300
 QY 301 IRORIILRFVATTHASEP 318
 DB 301 IRORIILRFVATTHASEP 318

RESULT 18

ABR54523 ID ABR54523 standard; protein; 318 AA.

XX ABR54523;

XX ABR54523;

DT 28-AUG-2003 (first entry)

XX Prostate tumour specific protein SEQ ID 920.
 XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;

KM Immune response; prostate cancer.

XX Homo sapiens.

XX WO200289747-A2.

PD 14-NOV-2002.

PF 09-MAY-2002; 2002WO-US014753.

XX 09-MAY-2001; 2001US-00852911.

PR 29-JUN-2001; 2001US-00895814.

PR 10-DEC-2001; 2001US-00012896.

XX (CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jhang Y, Henderson RA;

PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Veddyck TS;

PI Carter D, Li SX, Wang A, Skelky YAW, Hepler WT, Hural J;

PI McNeill PD, Houghton RL, Vinals Y De Baesolac, Foy TM, Watanabe Y;

PI Deng T;

DR WPI; 2003-167130/16.

XX Example 15; Page 638; 691pp; English.

XX The present invention relates to novel prostate-specific proteins (PSP)

CC and their coding sequences. The PSPs and their coding sequences are

CC useful for stimulating an immune response in a patient, or for treating

CC prostate cancer in a patient and for determining, detecting or diagnosing

CC the presence of a cancer in a patient. The present sequence was used to

CC illustrate the invention

XX Sequence 318 AA:

Query Match 99.8%; Score 1619; DB 6; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPCSLYLAVGNLTIIYVREHSLH 60
 DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPCSLYLAVGNLTIIYVREHSLH 60
 QY 61 PMYIFLCMSGIDILISTSMRPMKLAIFWNSSTTIQPDACLQIFAIHSLSGMESTVLLA 120
 DB 61 PMYIFLCMSGIDILISTSMRPMKLAIFWNSSTTIQPDACLQIFAIHSLSGMESTVLLA 120
 QY 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVGALMAMPVPFIKQLPFCRSNIIISHS 180
 DB 121 MAFDRYVAICHPLRHATVLTLPRTYKIGVAAVVGALMAMPVPFIKQLPFCRSNIIISHS 180
 QY 181 YCLHODVMKLAACDRIKVVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 DB 181 YCLHODVMKLAACDRIKVVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIIVPPIGISMVHRFSKRDSPLPVLIANIYLLVPPVLPVIYGVYTKS 300
 DB 241 GTCVSHCAVFIIVPPIGISMVHRFSKRDSPLPVLIANIYLLVPPVLPVIYGVYTKS 300
 QY 301 IRORIILRFVATTHASEP 318
 DB 301 IRORIILRFVATTHASEP 318

RESULT 19

ABP81974 ID ABP81974 standard; protein; 318 AA.

AC ABP81974;
XX
XX 04-MAR-2003 (first entry)
DE Human G protein-coupled receptor L853440 protein SEQ ID NO:434.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM G protein-coupled receptor modulator; antibody; immune-related disease;
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM immunological-related cell proliferative disease; autoimmune disease;
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM grief versus host disease; Parkinson's disease; multiple sclerosis; pain;
KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KM ulcer.
XX
XX Homo sapiens.
XX
XX WO200261087-A2.
XX
XX 08-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US050107.
XX
XX 19-DEC-2000; 2000US-0257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX Burner GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.
XX
XX N-PSDB; ABZ42822.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (1) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention
XX
XX Sequence 318 AA;

Query Match 99.8%; Score 1619; DB 6; Length 318;
Best Local Similarity 99.7%; Pred. No. 2,2e-169;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYDPNGNESSATYFILIGHGLEBAQFWLAPLCSLYLNAVGNLTIIYVTRHSLHS 60
DB 1 MMYDPNGNESSATYFILIGHGLEBAQFWLAPLCSLYLNAVGNLTIIYVTRHSLHS 60
QY 61 PMYFLCMGSDILISTSSMPKMLAFWNSTTIQPDACLLQFAIHSLSGMSSTYLLA 120
DB 61 PMYFLCMGSDILISTSSMPKMLAFWNSTTIQPDACLLQFAIHSLSGMSSTYLLA 120
QY 121 MAPRYVAICHPRLHATVLTLPYTKIGVAAVVGALMLAPLVFIQLPFCRSNIISHS 180
DB 121 MAPRYVAICHPRLHATVLTLPYTKIGVAAVVGALMLAPLVFIQLPFCRSNIISHS 180
QY 181 YCLHQDVMKLAACDIRVNVVYGLVIVISAIGLDLSLISFSYLLILKTVLGLTRBAQAKAF 240
DB 181 YCLHQDVMKLAACDIRVNVVYGLVIVISAIGLDLSLISFSYLLILKTVLGLTRBAQAKAF 240
QY 241 GTCVSHVCAVFIYPVPITGLSMVHRFSKRSDSPVPLANIYLLVPVLPVYGVYTKE 300
DB 241 GTCVSHVCAVFIYPVPITGLSMVHRFSKRSDSPVPLANIYLLVPVLPVYGVYTKE 300
QY 301 IRRRIILRFVATHASEP 318
DB 301 IRRRIILRFVATHASEP 318

RESULT 20
ADB14370
ID ADB14370 standard; protein; 318 AA.
XX
XX ADB14370;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human prostate specific protein P835P.
XX
XX Human; prostate specific cDNA; cytosolic; immunostimulant; gene therapy;
XX cell therapy; vaccine; T-cell epitope;
XX class I major histocompatibility complex allele; MHC; prostate cancer;
XX tumour; antigen presenting cell.
XX
XX Homo sapiens.
XX
XX US2003185830-A1.
XX
XX 02-OCT-2003.
XX
XX 12-NOV-2002; 2002US-00294025.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00232149.
XX 15-JAN-1999; 99US-00288946.
XX 09-APR-1999; 99US-00352616.
XX 13-JUL-1999; 99US-00439313.
XX 12-NOV-1999; 99US-00443686.
XX 18-NOV-1999; 99US-00483672.
XX 14-JAN-2000; 2000US-00536857.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.

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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:40:39 ; Search time 164 Seconds
(Without alignments)
810.181 Million cell updates/sec

Title: US-10-001-469a-2866
Perfect score: 1622
Sequence: 1 MWVDPNGNSSATYFILGL.....KEIRORILRLFHVATHASEP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodaca/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodaca/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubppaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodaca/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodaca/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1622	100.0	318	4	US-10-001-469-2880
2	1622	100.0	318	4	US-10-147-368-19
3	1622	100.0	318	4	US-10-147-368-28
4	1619	99.8	318	3	US-09-759-143-920
5	1619	99.8	318	3	US-09-780-669-920
6	1619	99.8	318	3	US-09-822-827-920
7	1619	99.8	318	3	US-09-886-055-91
8	1619	99.8	318	3	US-09-895-793-920
9	1619	99.8	318	3	US-09-895-814-920
10	1619	99.8	318	3	US-09-966-459A-2
11	1619	99.8	318	3	US-09-804-291-91
12	1619	99.8	318	4	US-10-012-896-920
13	1619	99.8	318	4	US-10-225-567A-434
14	1619	99.8	318	4	US-10-017-161-868
15	1619	99.8	318	4	US-10-144-678A-920
16	1619	99.8	318	4	US-10-294-025-920
17	1619	99.8	318	4	US-10-044-643-26
18	1619	99.8	318	4	US-10-147-368-32
19	1619	99.8	318	4	US-10-343-650A-158
20	1619	99.8	318	4	US-10-692-605-10
21	1619	99.8	318	4	US-10-323-412-2
22	1619	99.8	318	5	US-10-819-316-91
23	1617	99.7	317	4	US-10-205-823-443
24	1617	99.7	317	5	US-10-643-795A-125
25	1617	99.7	317	5	US-10-017-066-2
26	1617	99.7	317	5	US-10-948-518-125
27	1617	99.7	317	6	US-11-051-454-443

28	1614	99.5	317	4	US-10-295-027-873	Sequence 873, App
29	1614	99.5	317	4	US-10-292-798-746	Sequence 746, App
30	1614	99.4	318	4	US-10-044-643-28	Sequence 28, App
31	1612	99.4	318	4	US-10-044-643-30	Sequence 30, App
32	1610	99.3	316	4	US-10-147-368-33	Sequence 33, App
33	1542	95.1	303	4	US-10-001-469-2887	Sequence 2887, App
34	1534	94.6	302	4	US-10-001-469-2882	Sequence 2882, App
35	1515	93.4	298	4	US-10-001-469-2883	Sequence 2883, App
36	1515	93.4	298	4	US-10-001-469-2885	Sequence 2885, App
37	1515	93.4	298	4	US-10-147-368-35	Sequence 35, App
38	1515	93.4	298	4	US-10-147-368-37	Sequence 37, App
39	1512	93.2	316	4	US-10-147-368-34	Sequence 34, App
40	1512	93.2	317	5	US-10-774-355A-1329	Sequence 1329, App
41	1262	77.8	249	4	US-10-114-669-8894	Sequence 8894, App
42	985	60.7	320	4	US-10-005-041A-42	Sequence 42, App
43	985	60.7	320	5	US-10-774-355A-1347	Sequence 1347, App
44	979	60.4	318	4	US-10-024-399-18	Sequence 18, App
45	979	60.4	320	3	US-09-759-143-527	Sequence 527, App
46	979	60.4	320	3	US-09-730-018-7	Sequence 7, App
47	979	60.4	320	3	US-09-780-669-527	Sequence 527, App
48	979	60.4	320	3	US-09-822-827-527	Sequence 527, App
49	979	60.4	320	3	US-09-886-055-83	Sequence 83, App
50	979	60.4	320	3	US-09-968-033C-4	Sequence 4, App
51	979	60.4	320	3	US-09-895-793-527	Sequence 527, App
52	979	60.4	320	3	US-09-895-814-527	Sequence 527, App
53	979	60.4	320	3	US-09-804-291-83	Sequence 83, App
54	979	60.4	320	3	US-09-881-566A-55	Sequence 55, App
55	979	60.4	320	4	US-10-012-896-527	Sequence 527, App
56	979	60.4	320	4	US-10-081-775-4	Sequence 4, App
57	979	60.4	320	4	US-10-010-940-527	Sequence 527, App
58	979	60.4	320	4	US-10-205-823-337	Sequence 337, App
59	979	60.4	320	4	US-10-225-567A-662	Sequence 662, App
60	979	60.4	320	4	US-10-144-678A-527	Sequence 527, App
61	979	60.4	320	4	US-10-294-025-527	Sequence 527, App
62	979	60.4	320	4	US-10-431-842-7	Sequence 7, App
63	979	60.4	320	4	US-10-044-643-65	Sequence 65, App
64	979	60.4	320	4	US-10-025-806-34	Sequence 34, App
65	979	60.4	320	4	US-10-387-629-200	Sequence 200, App
66	979	60.4	320	4	US-10-005-041A-41	Sequence 41, App
67	979	60.4	320	4	US-10-343-650A-152	Sequence 152, App
68	979	60.4	320	5	US-10-968-294-4	Sequence 4, App
69	979	60.4	320	5	US-10-936-626-109	Sequence 109, App
70	979	60.4	320	5	US-10-938-061-109	Sequence 109, App
71	979	60.4	320	5	US-10-847-918-26	Sequence 26, App
72	979	60.4	320	5	US-10-819-316-83	Sequence 83, App
73	979	60.4	320	6	US-11-051-454-337	Sequence 337, App
74	979	60.4	368	4	US-10-106-698-6306	Sequence 6306, App
75	977.5	60.3	299	4	US-10-001-469-2886	Sequence 2886, App
76	977.5	60.3	299	4	US-10-147-368-38	Sequence 38, App
77	977	60.2	320	3	US-09-866-459A-12	Sequence 12, App
78	977	60.2	320	3	US-09-881-566A-53	Sequence 53, App
79	977	60.2	320	4	US-10-081-775-3	Sequence 3, App
80	977	60.2	320	4	US-10-044-643-64	Sequence 64, App
81	977	60.2	320	4	US-10-005-041A-44	Sequence 44, App
82	977	60.2	320	4	US-10-072-012-481	Sequence 481, App
83	977	60.2	320	4	US-10-323-412-12	Sequence 12, App
84	977	60.2	320	5	US-10-017-066-3	Sequence 3, App
85	975.5	60.1	299	4	US-10-001-469-2884	Sequence 2884, App
86	975.5	59.6	322	5	US-10-774-355A-12409	Sequence 123, App
87	967.5	59.6	322	5	US-10-017-066-4	Sequence 4, App
88	965.5	59.5	320	5	US-09-968-033C-2	Sequence 2, App
89	965.5	59.5	320	5	US-10-968-294-2	Sequence 2, App
90	964.5	59.5	320	4	US-10-079-719-2	Sequence 2, App
91	964.5	59.5	320	4	US-10-097-340-123	Sequence 123, App
92	964.5	59.5	320	4	US-10-387-629-38	Sequence 38, App
93	964.5	59.5	320	5	US-10-017-066-4	Sequence 4, App
94	964.5	59.5	320	6	US-11-050-926-123	Sequence 123, App
95	937.5	57.8	316	4	US-10-823-601-42	Sequence 42, App
96	937.5	57.8	324	3	US-09-886-055-81	Sequence 81, App
97	937.5	57.8	324	3	US-09-804-291-81	Sequence 81, App
98	937.5	57.8	324	4	US-10-023-601-14	Sequence 14, App
99	937.5	57.8	324	4	US-10-387-629-204	Sequence 204, App
100	937.5	57.8	324	4	US-10-292-798-832	Sequence 832, App

ALIGNMENTS

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RESULT 1
US-10-001-469-2880
; Sequence 2880, Application US/10001469
; Publication No. US20030091562A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: HUBERT, RENE
; APPLICANT: PARIS, MARY
; APPLICANT: CHALLITA-ELD, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 101P3A11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.20
; CURRENT APPLICATION NUMBER: US/10/001.469
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/680,728
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2888
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2880
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 101P3A11 encoded amino
; US-10-001-469-2880

Query Match      100.0%; Score 1622; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.7e-151;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFIILIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIYIVRTEHSLH 60
DB 1 MMVDPNGNESSATYFIILIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIYIVRTEHSLH 60
QY 61 PMYIFLCMSGIDILLISTSSMPKMLAIFWNSTTIQPDACLLQIPAHISLGSMESTVLLA 120
DB 61 PMYIFLCMSGIDILLISTSSMPKMLAIFWNSTTIQPDACLLQIPAHISLGSMESTVLLA 120
QY 121 MAPRKYAICHPRLHATVLTLPRTKIGVAAVVRGAAALMAPLVFPIKQLPFCRSNIIISHS 180
DB 121 MAPRKYAICHPRLHATVLTLPRTKIGVAAVVRGAAALMAPLVFPIKQLPFCRSNIIISHS 180
QY 121 YCLHQDVWKLACDDIRNVVYGLIIVISAGLDSLLISFSYLLILKTVLGLTREAOAKAF 240
DB 121 YCLHQDVWKLACDDIRNVVYGLIIVISAGLDSLLISFSYLLILKTVLGLTREAOAKAF 240
QY 181 YCLHQDVWKLACDDIRNVVYGLIIVISAGLDSLLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCLHQDVWKLACDDIRNVVYGLIIVISAGLDSLLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIYVPPFGLSMVHRFSKRSDPLPVLIANIYLLVPVLPNIYGVATKE 300
DB 241 GTCVSHVCAVFIYVPPFGLSMVHRFSKRSDPLPVLIANIYLLVPVLPNIYGVATKE 300
QY 301 IRORIILRFVHATASEP 318
DB 301 IRORIILRFVHATASEP 318
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```
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Paris
; APPLICANT: Arthur B. Raitano
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Douglas Saffran
; APPLICANT: Wangmao Ge
; APPLICANT: Pia M. Challita-Eld
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS
; TITLE OF INVENTION: ENTITLED 101P3A11 or PHOR-1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.21
; CURRENT APPLICATION NUMBER: US/10/147.368
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 10/017,066
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 10/001,469
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 09/680,728
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/157,902
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-147-368-19

Query Match      100.0%; Score 1622; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.7e-151;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFIILIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIYIVRTEHSLH 60
DB 1 MMVDPNGNESSATYFIILIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIYIVRTEHSLH 60
QY 61 PMYIFLCMSGIDILLISTSSMPKMLAIFWNSTTIQPDACLLQIPAHISLGSMESTVLLA 120
DB 61 PMYIFLCMSGIDILLISTSSMPKMLAIFWNSTTIQPDACLLQIPAHISLGSMESTVLLA 120
QY 121 MAPRKYAICHPRLHATVLTLPRTKIGVAAVVRGAAALMAPLVFPIKQLPFCRSNIIISHS 180
DB 121 MAPRKYAICHPRLHATVLTLPRTKIGVAAVVRGAAALMAPLVFPIKQLPFCRSNIIISHS 180
QY 121 YCLHQDVWKLACDDIRNVVYGLIIVISAGLDSLLISFSYLLILKTVLGLTREAOAKAF 240
DB 121 YCLHQDVWKLACDDIRNVVYGLIIVISAGLDSLLISFSYLLILKTVLGLTREAOAKAF 240
QY 181 YCLHQDVWKLACDDIRNVVYGLIIVISAGLDSLLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCLHQDVWKLACDDIRNVVYGLIIVISAGLDSLLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIYVPPFGLSMVHRFSKRSDPLPVLIANIYLLVPVLPNIYGVATKE 300
DB 241 GTCVSHVCAVFIYVPPFGLSMVHRFSKRSDPLPVLIANIYLLVPVLPNIYGVATKE 300
QY 301 IRORIILRFVHATASEP 318
DB 301 IRORIILRFVHATASEP 318

RESULT 3
US-10-147-368-28
; Sequence 28, Application US/10147368
; Publication No. US20030213004A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Paris
; APPLICANT: Arthur B. Raitano
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Douglas Saffran
; APPLICANT: Wangmao Ge
```


! CURRENT APPLICATION NUMBER: US/09/780,669
! CURRENT FILING DATE: 2001-02-09
! NUMBER OF SEQ ID NOS: 943
! SOFTWARE: PaateSeq for Windows Version 3.0
! SEQ ID NO 920
! LENGTH: 318
! TYPE: PRT
! ORGANISM: Homo sapiens
US-09-780-669-920

Query Match 99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIIVYVREHSLHE 60
DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIIVYVREHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQPDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQPDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAEDRYVAICHPLRHAATVLTLPRTYKIGVAAVVRGAALMAELPVFIIKQLPFCRSNIISHS 180
DB 121 MAEDRYVAICHPLRHAATVLTLPRTYKIGVAAVVRGAALMAELPVFIIKQLPFCRSNIISHS 180
QY 181 YCHLQDVMKLCACDDIRNVVYGLVITISAGLDSILISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCHLQDVMKLCACDDIRNVVYGLVITISAGLDSILISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLANPIYVGVTKE 300
DB 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLANPIYVGVTKE 300
QY 301 IRQRILRLFHVATASEP 318
DB 301 IRQRILRLFHVATASEP 318

RESULT 6
US-09-822-827-920
! Sequence 920, Application US/09822827
! Patent No. US20020081680A1
! GENERAL INFORMATION:
! APPLICANT: Xu, Jiansheng
! TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
! TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
! FILE REFERENCE: 210121.534C1
! CURRENT APPLICATION NUMBER: US/09/822,827
! CURRENT FILING DATE: 2001-03-28
! NUMBER OF SEQ ID NOS: 982
! SOFTWARE: PaateSeq for Windows Version 3.0
! SEQ ID NO 920
! LENGTH: 318
! TYPE: PRT
! ORGANISM: Homo sapiens
US-09-822-827-920

Query Match 99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIIVYVREHSLHE 60
DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIIVYVREHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQPDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQPDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAEDRYVAICHPLRHAATVLTLPRTYKIGVAAVVRGAALMAELPVFIIKQLPFCRSNIISHS 180
DB 121 MAEDRYVAICHPLRHAATVLTLPRTYKIGVAAVVRGAALMAELPVFIIKQLPFCRSNIISHS 180

QY 181 YCHLQDVMKLCACDDIRNVVYGLVITISAGLDSILISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCHLQDVMKLCACDDIRNVVYGLVITISAGLDSILISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLANPIYVGVTKE 300
DB 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLANPIYVGVTKE 300
QY 301 IRQRILRLFHVATASEP 318
DB 301 IRQRILRLFHVATASEP 318

RESULT 7
US-09-886-055-91
! Sequence 91, Application US/09886055
! Patent No. US20020132273A1
! GENERAL INFORMATION:
! APPLICANT: STRYER, LUBERT
! APPLICANT: ZOZULYA, SERGEY
! TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
! TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
! FILE REFERENCE: 078003-0277150
! CURRENT APPLICATION NUMBER: US/09/886,055
! CURRENT FILING DATE: 2001-06-22
! PRIOR APPLICATION NUMBER: 60/213,812
! PRIOR FILING DATE: 2000-06-22
! NUMBER OF SEQ ID NOS: 522
! SOFTWARE: PatentIn Ver. 2.1
! SEQ ID NO 91
! LENGTH: 318
! TYPE: PRT
! ORGANISM: Homo sapiens
US-09-886-055-91

Query Match 99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIIVYVREHSLHE 60
DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIVAGNLTIIVYVREHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQPDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWENSTTIQPDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAEDRYVAICHPLRHAATVLTLPRTYKIGVAAVVRGAALMAELPVFIIKQLPFCRSNIISHS 180
DB 121 MAEDRYVAICHPLRHAATVLTLPRTYKIGVAAVVRGAALMAELPVFIIKQLPFCRSNIISHS 180
QY 181 YCHLQDVMKLCACDDIRNVVYGLVITISAGLDSILISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCHLQDVMKLCACDDIRNVVYGLVITISAGLDSILISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLANPIYVGVTKE 300
DB 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLANPIYVGVTKE 300
QY 301 IRQRILRLFHVATASEP 318
DB 301 IRQRILRLFHVATASEP 318

RESULT 8
US-09-895-793-920
! Sequence 920, Application US/09895793
! Publication No. US20020192763A1
! GENERAL INFORMATION:
! APPLICANT: Xu, Jiansheng
! APPLICANT: Dillon, Devin C.
! APPLICANT: Mitcham, Jennifer L.


```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugtu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-793-920

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Query Match          99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYDPNGNESSATYFIIIGLPGLEBAQFWLAPLCSLYLAVGNLTIIYVTRHSLH 60
DB 1 MMYDPNGNESSATYFIIIGLPGLEBAQFWLAPLCSLYLAVGNLTIIYVTRHSLH 60

QY 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAHISLGSBESTVLLA 120
DB 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAHISLGSBESTVLLA 120

QY 121 MAFDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLVFPIKQLPFCRSNIIISHS 180
DB 121 MAFDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLVFPIKQLPFCRSNIIISHS 180

QY 181 YCHODVMKACDIDIRNVVYGLIIVISAGLDSLISFSYLLIKTVLGLTREBAQKAF 240
DB 181 YCHODVMKACDIDIRNVVYGLIIVISAGLDSLISFSYLLIKTVLGLTREBAQKAF 240

QY 241 GTCVSHVCAVFITYVPPIGSMVHRFSKRDSPLVILANIYLLVPPVLPVIYGVYTKK 300
DB 241 GTCVSHVCAVFITYVPPIGSMVHRFSKRDSPLVILANIYLLVPPVLPVIYGVYTKK 300

QY 301 IRRRIILRFHVATHASEP 318
DB 301 IRRRIILRFHVATHASEP 318

```

```

RESULT 9
US-09-895-814-920
; Sequence 920, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugtu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.

```

```

; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-814-920

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Query Match          99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYDPNGNESSATYFIIIGLPGLEBAQFWLAPLCSLYLAVGNLTIIYVTRHSLH 60
DB 1 MMYDPNGNESSATYFIIIGLPGLEBAQFWLAPLCSLYLAVGNLTIIYVTRHSLH 60

QY 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAHISLGSBESTVLLA 120
DB 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAHISLGSBESTVLLA 120

QY 121 MAFDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLVFPIKQLPFCRSNIIISHS 180
DB 121 MAFDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLVFPIKQLPFCRSNIIISHS 180

QY 181 YCHODVMKACDIDIRNVVYGLIIVISAGLDSLISFSYLLIKTVLGLTREBAQKAF 240
DB 181 YCHODVMKACDIDIRNVVYGLIIVISAGLDSLISFSYLLIKTVLGLTREBAQKAF 240

QY 241 GTCVSHVCAVFITYVPPIGSMVHRFSKRDSPLVILANIYLLVPPVLPVIYGVYTKK 300
DB 241 GTCVSHVCAVFITYVPPIGSMVHRFSKRDSPLVILANIYLLVPPVLPVIYGVYTKK 300

QY 301 IRRRIILRFHVATHASEP 318
DB 301 IRRRIILRFHVATHASEP 318

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RESULT 10
US-09-966-459A-2
; Sequence 2, Application US/0966459A
; Publication No. US2003002237A1
; GENERAL INFORMATION:
; APPLICANT: FESDER, J.N.
; APPLICANT: MINTER, G.
; APPLICANT: RAMANATHAN, C.S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CACACE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNAKNER, M.G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRMY4,
; FILE REFERENCE: D0039NP
; CURRENT APPLICATION NUMBER: US/09/966,459A

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; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,833
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,776
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/305,351
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,202
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 318
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-966-459A.2

Query Match          99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3,4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIIVYVREHSLHE 60
DB 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIIVYVREHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQFDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQFDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHATVTLPRVTKIGVAAVRGAAALMAPLPVFIKQLPFCRSNIIISHS 180
DB 121 MAFDRYVAICHPLRHATVTLPRVTKIGVAAVRGAAALMAPLPVFIKQLPFCRSNIIISHS 180
QY 181 YCLHODVMKLAACDRIRVNVVYGLVIIISALGLDLSLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCLHODVMKLAACDRIRVNVVYGLVIIISALGLDLSLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHCAVFIFFVPIFGLSMVRFSKRSDPLPVILANIYLLVPPVLPNIYVGVYKTK 300
DB 241 GTCVSHCAVFIFFVPIFGLSMVRFSKRSDPLPVILANIYLLVPPVLPNIYVGVYKTK 300
QY 301 IRRILRLFHVATHASEP 318
DB 301 IRRILRLFHVATHASEP 318

RESULT 11
US-09-804-291-91
; Sequence 91, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZILA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
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; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 318
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-804-291-91

Query Match          99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3,4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIIVYVREHSLHE 60
DB 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIIVYVREHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQFDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQFDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHATVTLPRVTKIGVAAVRGAAALMAPLPVFIKQLPFCRSNIIISHS 180
DB 121 MAFDRYVAICHPLRHATVTLPRVTKIGVAAVRGAAALMAPLPVFIKQLPFCRSNIIISHS 180
QY 181 YCLHODVMKLAACDRIRVNVVYGLVIIISALGLDLSLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCLHODVMKLAACDRIRVNVVYGLVIIISALGLDLSLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHCAVFIFFVPIFGLSMVRFSKRSDPLPVILANIYLLVPPVLPNIYVGVYKTK 300
DB 241 GTCVSHCAVFIFFVPIFGLSMVRFSKRSDPLPVILANIYLLVPPVLPNIYVGVYKTK 300
QY 301 IRRILRLFHVATHASEP 318
DB 301 IRRILRLFHVATHASEP 318

RESULT 12
US-10-012-896-920
; Sequence 920, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalow, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Baesols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
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SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 920
 LENGTH: 318
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-012-896-920

Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. No. 3.4e-151;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLVANGLNTIIVYVTEHSLHE 60
 DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLVANGLNTIIVYVTEHSLHE 60
 QY 61 PMYIFLCMISGIDILISTSSMPKMLAIFWNSSTTIQPDACLLQFAHSLSGMESTVLLA 120
 DB 61 PMYIFLCMISGIDILISTSSMPKMLAIFWNSSTTIQPDACLLQFAHSLSGMESTVLLA 120
 QY 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
 DB 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
 QY 181 YCLHODVWKLACDDIRVNVVYGLVIVISAGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 DB 181 YCLHODVWKLACDDIRVNVVYGLVIVISAGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIYVPFPIGLSMVHRSKRSDPLVILANIYLLVPPVLANPIYVGVTKE 300
 DB 241 GTCVSHCAVFIYVPFPIGLSMVHRSKRSDPLVILANIYLLVPPVLANPIYVGVTKE 300
 QY 301 IRRRIILRFHVATASEP 318
 DB 301 IRRRIILRFHVATASEP 318

RESULT 13
 US-10-225-567A-434
 Sequence 434, Application US/10225567A
 Publication No. US20030113798A1
 GENERAL INFORMATION:
 APPLICANT: Lifespan Biosciences
 APPLICANT: Burnet, Glenn P.
 APPLICANT: Roush, Christine L.
 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 1920-4-4
 CURRENT APPLICATION NUMBER: US/10/225,567A
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/257,144
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 2292
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 434
 LENGTH: 318
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-225-567A-434

Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. No. 3.4e-151;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLVANGLNTIIVYVTEHSLHE 60
 DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLVANGLNTIIVYVTEHSLHE 60
 QY 61 PMYIFLCMISGIDILISTSSMPKMLAIFWNSSTTIQPDACLLQFAHSLSGMESTVLLA 120
 DB 61 PMYIFLCMISGIDILISTSSMPKMLAIFWNSSTTIQPDACLLQFAHSLSGMESTVLLA 120
 QY 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
 DB 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180

DB 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
 QY 181 YCLHODVWKLACDDIRVNVVYGLVIVISAGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 DB 181 YCLHODVWKLACDDIRVNVVYGLVIVISAGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIYVPFPIGLSMVHRSKRSDPLVILANIYLLVPPVLANPIYVGVTKE 300
 DB 241 GTCVSHCAVFIYVPFPIGLSMVHRSKRSDPLVILANIYLLVPPVLANPIYVGVTKE 300
 QY 301 IRRRIILRFHVATASEP 318
 DB 301 IRRRIILRFHVATASEP 318

RESULT 14
 US-10-017-161-868
 Sequence 868, Application US/10017161
 Publication No. US20030143668A1
 GENERAL INFORMATION:
 APPLICANT: SUMA, MAKIKO
 APPLICANT: ASAI, KIYOSHI
 APPLICANT: AKIYAMA, YUTAKA
 APPLICANT: ABEYATANI, HIROYUKI
 TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 084335/0152
 CURRENT APPLICATION NUMBER: US/10/017,161
 PRIOR FILING DATE: 2002-12-18
 PRIOR APPLICATION NUMBER: JP 2001/246789
 PRIOR FILING DATE: 2001-06-18
 NUMBER OF SEQ ID NOS: 2430
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 868
 LENGTH: 318
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-017-161-868

Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. No. 3.4e-151;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLVANGLNTIIVYVTEHSLHE 60
 DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLVANGLNTIIVYVTEHSLHE 60
 QY 61 PMYIFLCMISGIDILISTSSMPKMLAIFWNSSTTIQPDACLLQFAHSLSGMESTVLLA 120
 DB 61 PMYIFLCMISGIDILISTSSMPKMLAIFWNSSTTIQPDACLLQFAHSLSGMESTVLLA 120
 QY 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
 DB 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
 QY 181 YCLHODVWKLACDDIRVNVVYGLVIVISAGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 DB 181 YCLHODVWKLACDDIRVNVVYGLVIVISAGLDSLISFSYLLILKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIYVPFPIGLSMVHRSKRSDPLVILANIYLLVPPVLANPIYVGVTKE 300
 DB 241 GTCVSHCAVFIYVPFPIGLSMVHRSKRSDPLVILANIYLLVPPVLANPIYVGVTKE 300
 QY 301 IRRRIILRFHVATASEP 318
 DB 301 IRRRIILRFHVATASEP 318

RESULT 15
 US-10-144-678A-920
 Sequence 920, Application US/10144678A
 Publication No. US20030157089A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jlangchun

APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kaios, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William T.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Basols, Carlotca
APPLICANT: Foy, Teresa M.
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PR
ORGANISM: Homo sapiens
US-10-144-678A-920

Query Match 99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIILIGLPGBEAQFWLAFPLCSLYLAVGNLTITTYIVRTEHSIHE 60
DB 1 MMVDPNNGESSATYFIILIGLPGBEAQFWLAFPLCSLYLAVGNLTITTYIVRTEHSIHE 60
QY 61 PMYIFLCMLSGDILISTSSMPKMLAFWNSTTIQFDACLLQWFAHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGDILISTSSMPKMLAFWNSTTIQFDACLLQWFAHSLSGMESTVLLA 120
QY 121 MAPDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISSHS 180
DB 121 MAPDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISSHS 180
QY 181 YCHQDVKWKLACDDIRVNVVGLIYISALIGDSLISFSYLLIKTVLGLTREAOAKAF 240
DB 181 YCHQDVKWKLACDDIRVNVVGLIYISALIGDSLISFSYLLIKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIYVPFIGLSMVHRFSKRSDPLVILANTYLLVPLNPIVGVKTKX 300
DB 241 GTCVSHVCAVFIYVPFIGLSMVHRFSKRSDPLVILANTYLLVPLNPIVGVKTKX 300
QY 301 IRRRIILRLFHVATASEP 318
DB 301 IRRRIILRLFHVATASEP 318

RESULT 16
US-10-294-025-920
Sequence 920, Application US/10294025
Publication No. US20030185630A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiaqun
APPLICANT: Stolk, John A.
APPLICANT: Kaios, Michael D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PR
ORGANISM: Homo sapiens
US-10-294-025-920

Query Match 99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIILIGLPGBEAQFWLAFPLCSLYLAVGNLTITTYIVRTEHSIHE 60
DB 1 MMVDPNNGESSATYFIILIGLPGBEAQFWLAFPLCSLYLAVGNLTITTYIVRTEHSIHE 60
QY 61 PMYIFLCMLSGDILISTSSMPKMLAFWNSTTIQFDACLLQWFAHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGDILISTSSMPKMLAFWNSTTIQFDACLLQWFAHSLSGMESTVLLA 120
QY 121 MAPDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISSHS 180
DB 121 MAPDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISSHS 180
QY 181 YCHQDVKWKLACDDIRVNVVGLIYISALIGDSLISFSYLLIKTVLGLTREAOAKAF 240
DB 181 YCHQDVKWKLACDDIRVNVVGLIYISALIGDSLISFSYLLIKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIYVPFIGLSMVHRFSKRSDPLVILANTYLLVPLNPIVGVKTKX 300
DB 241 GTCVSHVCAVFIYVPFIGLSMVHRFSKRSDPLVILANTYLLVPLNPIVGVKTKX 300
QY 301 IRRRIILRLFHVATASEP 318
DB 301 IRRRIILRLFHVATASEP 318

RESULT 17
US-10-044-643-26
Sequence 26, Application US/10044643
Publication No. US20030195335A1
GENERAL INFORMATION:
APPLICANT: Majumder, Kumud
APPLICANT: Vernier, Corine
APPLICANT: Caeman, Stacie J
APPLICANT: Wolenc, Adam R
APPLICANT: Spaderna, Steven K
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu S
APPLICANT: Tchernev, Velizar T
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Baumgartner, Jason C
APPLICANT: Guev, Vladimir
TITLE OF INVENTION: No. US20030195335A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-748
CURRENT APPLICATION NUMBER: US/10/044,643
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 60/193,664
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/194,614
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,063
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,066
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,067
PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 60/195,068
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,069
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,070
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,510
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/219,855
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/221,284
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/221,325
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/224,588
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/239,613
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/262,508
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/263,604
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,433
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/265,161
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-044-643-26

Query Match 99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MMDPNBESSATYFLLIGLGLBEAOFMLAFPLCSYLLAVGNLTITTYVREHSLHE 60
1 MMDPNBESSATYFLLIGLGLBEAOFMLAFPLCSYLLAVGNLTITTYVREHSLHE 60
61 PMYIFLCMLSGIDILISTSMFKMLAFWENSTTIQPDACILQIFAIHSHSGMESTVLLA 120
61 PMYIFLCMLSGIDILISTSMFKMLAFWENSTTIQPDACILQIFAIHSHSGMESTVLLA 120
121 MAFDRYVAICHPRLHATVTLPRVTXIGVAAVVRGALMALPVPFIKQLPFCRSNIISHS 180
121 MAFDRYVAICHPRLHATVTLPRVTXIGVAAVVRGALMALPVPFIKQLPFCRSNIISHS 180
121 MAFDRYVAICHPRLHATVTLPRVTXIGVAAVVRGALMALPVPFIKQLPFCRSNIISHS 180
181 YCHLHODVMKLAACDIRNVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
181 YCHLHODVMKLAACDIRNVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
241 GTCVSHCAVFIFVPPFISGMVHRFSKRDSPLPVLINITYLLVPPVLPVIYGVYTKS 300
241 GTCVSHCAVFIFVPPFISGMVHRFSKRDSPLPVLINITYLLVPPVLPVIYGVYTKS 300
301 IRORIILRLFHVATHASEP 318
301 IRORIILRLFHVATHASEP 318

RESULT 18
US-10-147-368-32
Sequence 32, Application US/10147368
Publication No. US20030233004A1
GENERAL INFORMATION:
APPLICANT: Agemey, Inc.
APPLICANT: Aya Jakobovits
APPLICANT: Mary Paris
APPLICANT: Archur B. Raitano
APPLICANT: Robert Kendall Morrison

APPLICANT: Douglas Saffran
APPLICANT: Wangmao Ge
APPLICANT: Pia M. Chailita-Eid
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS
TITLE OF INVENTION: ENTITLED 101P3A11 OR PHOR-1 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20024.21
CURRENT APPLICATION NUMBER: US/10/147,368
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US 10/017,066
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 10/001,469
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US 60/291,118
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 09/680,728
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: US 60/157,902
PRIOR FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 47
SOFTWARE: RascSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 318
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-147-368-32

Query Match 99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MMDPNBESSATYFLLIGLGLBEAOFMLAFPLCSYLLAVGNLTITTYVREHSLHE 60
1 MMDPNBESSATYFLLIGLGLBEAOFMLAFPLCSYLLAVGNLTITTYVREHSLHE 60
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61 PMYIFLCMLSGIDILISTSMFKMLAFWENSTTIQPDACILQIFAIHSHSGMESTVLLA 120
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121 MAFDRYVAICHPRLHATVTLPRVTXIGVAAVVRGALMALPVPFIKQLPFCRSNIISHS 180
121 MAFDRYVAICHPRLHATVTLPRVTXIGVAAVVRGALMALPVPFIKQLPFCRSNIISHS 180
181 YCHLHODVMKLAACDIRNVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
181 YCHLHODVMKLAACDIRNVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
241 GTCVSHCAVFIFVPPFISGMVHRFSKRDSPLPVLINITYLLVPPVLPVIYGVYTKS 300
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301 IRORIILRLFHVATHASEP 318
301 IRORIILRLFHVATHASEP 318

RESULT 19
US-10-343-650A-158
Sequence 158, Application US/10343650A
Publication No. US20040067499A1
GENERAL INFORMATION:
APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 158

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; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-158

Query Match      99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFLPCSLYLIAVGNLTIIYIVRTEHSLHE 60

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   |||||
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSTTIQPDACILQWFAHSLSGMESTVLLA 120

QY 121 MAPDRYVAICHPLRHATVLTLPVTKIGVAAVVGAALMAPLPVFIKQLPFCRSNIISHS 180
   |||||
DB 121 MAPDRYVAICHPLRHATVLTLPVTKIGVAAVVGAALMAPLPVFIKQLPFCRSNIISHS 180

QY 181 YCLHODVMKLAACDDIRVVNVYGLVVIISAIGLSLISFSYLLIKTVLGLTREAOAKAF 240
   |||||
DB 181 YCLHODVMKLAACDDIRVVNVYGLVVIISAIGLSLISFSYLLIKTVLGLTREAOAKAF 240

QY 241 GTCVSHVCAVFIFFVPPFISLMSVHRSKRSDSPPLVILANIYLLVPPVLANPIYVGVTKE 300
   |||||
DB 241 GTCVSHVCAVFIFFVPPFISLMSVHRSKRSDSPPLVILANIYLLVPPVLANPIYVGVTKE 300

QY 301 IRORILRLFHVATHASEP 318
   |||||
DB 301 IRORILRLFHVATHASEP 318
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RESULT 20
US-10-692-605-10
; Sequence 10, Application US/10692605
; Publication No. US20040091928A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S.
; APPLICANT: Merchant, Kalpana
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
; FILE REFERENCE: 28341/6276.NX1
; CURRENT APPLICATION NUMBER: US/10/692,605
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US 09/698,419
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 09/481,794
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 09/454,399
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 09/429,517
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,555
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,676
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,695
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/428,114
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/428,020
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/427,859
; PRIOR FILING DATE: 1999-10-27
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-692-605-10

Query Match      99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFLPCSLYLIAVGNLTIIYIVRTEHSLHE 60
   |||||
DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFLPCSLYLIAVGNLTIIYIVRTEHSLHE 60

QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSTTIQPDACILQWFAHSLSGMESTVLLA 120
   |||||
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSTTIQPDACILQWFAHSLSGMESTVLLA 120

QY 121 MAPDRYVAICHPLRHATVLTLPVTKIGVAAVVGAALMAPLPVFIKQLPFCRSNIISHS 180
   |||||
DB 121 MAPDRYVAICHPLRHATVLTLPVTKIGVAAVVGAALMAPLPVFIKQLPFCRSNIISHS 180

QY 181 YCLHODVMKLAACDDIRVVNVYGLVVIISAIGLSLISFSYLLIKTVLGLTREAOAKAF 240
   |||||
DB 181 YCLHODVMKLAACDDIRVVNVYGLVVIISAIGLSLISFSYLLIKTVLGLTREAOAKAF 240

QY 241 GTCVSHVCAVFIFFVPPFISLMSVHRSKRSDSPPLVILANIYLLVPPVLANPIYVGVTKE 300
   |||||
DB 241 GTCVSHVCAVFIFFVPPFISLMSVHRSKRSDSPPLVILANIYLLVPPVLANPIYVGVTKE 300

QY 301 IRORILRLFHVATHASEP 318
   |||||
DB 301 IRORILRLFHVATHASEP 318
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Search completed: March 9, 2006, 08:43:56
Job time : 166 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2006, 08:41:19 ; Search time 22 Seconds
(without alignments)
402.341 Million cell updates/sec

Title: US-10-001-469A-2866

Perfect score: 1622
Sequence: 1 MWMDPNGESSATYFILIGL.....KEIRQRIRLRFVATASEP 318

Scoring table:

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Gapop 10.0 , Gapect 0.5

Searched: 161667 seqs, 2783485 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA New:*
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2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubppaa/PTCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubppaa/USC0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	979	60.4	320	7	US-11-234-786-527
2	892.5	55.0	329	6	US-10-055-877-336
3	868.5	53.5	312	6	US-10-055-877-339
4	827.5	51.0	315	7	US-11-190-188-8
5	812.5	50.1	342	6	US-10-511-538-70
6	799.5	49.3	344	6	US-10-055-877-335
7	771	47.5	311	7	US-11-190-188-10
8	758.5	46.8	321	6	US-10-055-877-338
9	742	45.7	356	7	US-11-190-188-9
10	737.5	45.5	312	7	US-11-124-367A-496
11	736.5	45.4	312	7	US-11-124-367A-514
12	726.5	44.8	303	6	US-10-055-877-123
13	718.5	44.3	327	6	US-10-055-877-337
14	648	40.0	321	6	US-10-511-538-225
15	494.5	30.5	312	6	US-10-511-538-34
16	475	29.3	318	6	US-10-055-877-322
17	475	29.3	319	6	US-10-055-877-326
18	464	28.6	319	6	US-10-055-877-224
19	464	28.6	319	7	US-11-190-188-12
20	463	28.5	319	6	US-10-511-538-21
21	459.5	28.3	318	6	US-10-055-877-220
22	459.5	28.3	318	6	US-10-055-877-225
23	451.5	27.8	319	6	US-10-055-877-223
24	447.5	27.6	314	6	US-10-055-877-56
25	443.5	27.3	319	6	US-10-055-877-221

26	442.5	27.3	318	6	US-10-055-877-324	Sequence 324, App
27	442	27.1	311	6	US-10-511-538-176	Sequence 176, App
28	439.5	27.1	453	7	US-11-190-188-19	Sequence 19, App
29	435.5	26.8	318	6	US-10-055-877-323	Sequence 323, App
30	429.5	26.5	315	7	US-11-241-956-15	Sequence 15, App
31	429.5	26.5	491	6	US-10-511-538-48	Sequence 48, App
32	427.5	26.4	312	7	US-11-241-956-12	Sequence 12, App
33	426.5	26.3	315	7	US-11-241-956-11	Sequence 11, App
34	419.5	25.9	314	6	US-10-511-538-153	Sequence 153, App
35	418	25.8	309	7	US-11-241-956-13	Sequence 13, App
36	411.5	25.4	311	7	US-11-190-188-15	Sequence 15, App
37	409.5	25.2	313	7	US-11-095-093-2	Sequence 2, App
38	407	25.1	310	6	US-10-511-538-215	Sequence 215, App
39	406.5	25.1	310	7	US-11-190-188-14	Sequence 14, App
40	405.5	25.0	312	7	US-11-124-368A-330	Sequence 330, App
41	405.5	25.0	312	7	US-10-055-877-62	Sequence 62, App
42	400.5	24.7	307	6	US-10-055-877-232	Sequence 232, App
43	400.5	24.7	307	6	US-10-055-877-232	Sequence 13, App
44	400.5	24.7	309	7	US-11-190-188-13	Sequence 13, App
45	400.5	24.7	318	6	US-10-055-877-119	Sequence 119, App
46	400.5	24.7	318	6	US-10-055-877-322	Sequence 322, App
47	399.5	24.6	310	6	US-10-511-538-217	Sequence 217, App
48	396	24.4	308	6	US-10-055-877-235	Sequence 235, App
49	395	24.4	318	6	US-10-511-538-163	Sequence 163, App
50	395	24.4	318	7	US-11-190-188-21	Sequence 21, App
51	394.5	24.3	326	6	US-10-511-538-186	Sequence 186, App
52	393	24.2	316	7	US-11-190-188-18	Sequence 18, App
53	390	24.0	313	7	US-11-190-188-7	Sequence 7, App
54	388.5	24.0	346	7	US-11-190-188-17	Sequence 17, App
55	387	23.9	308	6	US-10-055-877-233	Sequence 233, App
56	387	23.8	313	6	US-10-055-877-234	Sequence 234, App
57	386.5	23.8	307	7	US-11-241-956-16	Sequence 16, App
58	386.5	23.8	312	6	US-10-511-538-97	Sequence 97, App
59	383.5	23.6	309	6	US-10-511-538-188	Sequence 188, App
60	376	23.2	313	6	US-10-511-538-64	Sequence 64, App
61	374	23.1	277	6	US-10-055-877-236	Sequence 236, App
62	370	22.8	314	7	US-11-190-188-16	Sequence 16, App
63	365.5	22.5	306	6	US-10-511-538-182	Sequence 182, App
64	353.5	21.8	323	6	US-10-511-538-168	Sequence 168, App
65	353.5	21.8	333	7	US-11-190-188-20	Sequence 20, App
66	351	21.6	308	6	US-10-511-538-219	Sequence 219, App
67	344.5	21.2	313	6	US-10-511-538-13	Sequence 13, App
68	332	20.5	268	6	US-10-511-538-7	Sequence 7, App
69	309	19.5	354	7	US-11-190-188-11	Sequence 11, App
70	308	19.0	309	7	US-11-241-956-14	Sequence 14, App
71	262	16.2	280	6	US-10-511-538-2	Sequence 2, App
72	248	15.3	264	6	US-10-511-538-41	Sequence 41, App
73	184.5	11.4	317	6	US-10-995-561-798	Sequence 78, App
74	184.5	11.4	318	7	US-11-127-877-38	Sequence 38, App
75	184.5	11.4	797	6	US-10-995-561-802	Sequence 802, App
76	183.5	11.3	173	6	US-10-511-538-190	Sequence 190, App
77	180	11.1	335	7	US-11-166-412-65	Sequence 65, App
78	174.5	10.8	350	6	US-10-995-561-547	Sequence 547, App
79	161	9.9	144	7	US-11-000-463-376	Sequence 376, App
80	160.5	9.9	360	6	US-10-959-310-36	Sequence 36, App
81	160.5	9.9	360	7	US-11-144-731-1	Sequence 1, App
82	159	9.8	367	7	US-11-174-816-42	Sequence 42, App
83	159	9.8	347	7	US-11-174-819-9	Sequence 9, App
84	158	9.7	359	6	US-10-330-773-930	Sequence 930, App
85	156	9.6	259	6	US-10-055-877-225	Sequence 225, App
86	156	9.6	259	6	US-10-055-877-237	Sequence 237, App
87	156	9.6	259	7	US-11-206-587-27	Sequence 27, App
88	156	9.6	259	7	US-11-206-587-29	Sequence 29, App
89	156	9.6	412	7	US-11-170-153-4	Sequence 4, App
90	156	9.6	412	7	US-11-170-166-4	Sequence 4, App
91	156	9.6	412	7	US-11-170-351-1	Sequence 1, App
92	156	9.6	415	7	US-11-170-153-2	Sequence 2, App
93	156	9.6	415	7	US-11-170-166-2	Sequence 2, App
94	156	9.6	415	7	US-11-170-351-2	Sequence 2, App
95	155	9.6	347	7	US-11-174-816-57	Sequence 57, App
96	155	9.6	347	7	US-11-174-819-76	Sequence 76, App
97	154	9.5	361	6	US-10-987-856-16	Sequence 16, App
98	153	9.4	360	6	US-10-851-667A-26	Sequence 26, App

APPLICANT: YAO, Montique G.
APPLICANT: SHIH, Leo L.
APPLICANT: TRIBOULEY, Catherine
APPLICANT: LU, Dzung Aina M.
APPLICANT: YUE, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: POLICKI, Jennifer L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: YANG, Junning
APPLICANT: HARLAND, Lee
APPLICANT: WALSH, Roderick T.
APPLICANT: LO, Terence P.
APPLICANT: BOROWSKY, Mark L.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0044 PCT
CURRENT APPLICATION NUMBER: US/11/190,188
CURRENT FILING DATE: 2005-07-27
PRIOR APPLICATION NUMBER: US/10/220,382
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 8
LENGTH: 315
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7472361CD1
US-11-190-188-8

Query Match 51.0%; Score 827.5; DB 7; Length 315;
Best Local Similarity 49.8%; Pred. No. 2,1e-68;

Matches 154; Conservative 64; Mismatches 90; Indels 1; Gaps 1;

QY 2 MVDNNGSSATYFILGLPGLEAQLAPPLCSLYLAVLGNLTIIYVTERSHLEP 61
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QY 62 MYTLCMLSGDILISTSSMRMLAIFPNSTTIOFDACLOIPAIHLSGMSVYLLAM 121
DB 61 MYTISILAVNDLGSSTLPTMLAVLWDAPEIQASACVQOLFPIHFTPLSSVLLAM 120
QY 122 AFDYVVAICHPRLRATVTLTLPRTKIGVAAVVRGAALMAPLPVFIKQDPFGSNLSHSY 181
DB 121 AFDPRVAICHPRLRATVTLTLPRTKIGVAAVVRGAALMAPLPVFIKQDPFGSNLSHSY 180
QY 182 CLHODVMKLACDDIRVNVVYGLVYIISAGLSLISFSYLLIKTVLGL-TREAQAKAF 240
DB 181 CLHODVRLKSTCDARTNSIYGLCVAVIATLGVDSIFILSYVLIANTVLDIASREQLKAL 240
QY 241 GTCVSHVCAVPIFYVPGISGMWRHRSKRDSPLPVILANITYLVLPPLANIVGVTKKE 300
DB 241 NTCVSHICVAVIIFVYVIGVSMWRHFGHLSPIVHILMADIVLLPVLNPIVYSVRTKQ 300
QY 301 IRRGRLRLP 309
DB 301 IRLGILHKL 309

RESULT 5
US-10-511-538-70
Sequence 70, Application US/10511538
Publication No. US20060026700A1
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
FILE REFERENCE: 16U 200 PCT
CURRENT APPLICATION NUMBER: US/10/511,538
CURRENT FILING DATE: 2004-10-18
PRIOR APPLICATION NUMBER: US 60/372,669
PRIOR FILING DATE: 2002-04-16

PRIOR APPLICATION NUMBER: US 60/411,882
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US 60/424,336
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: US 60/374,823
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 60/376,558
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: US 60/381,366
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 60/403,648
PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PatentIn version 3.1
SEQ ID NO 70
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-538-70

Query Match 50.1%; Score 812.5; DB 6; Length 314;
Best Local Similarity 50.7%; Pred. No. 4.9e-67;

Matches 151; Conservative 59; Mismatches 87; Indels 1; Gaps 1;

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DB 12 TAPLVGIPGLEHLMHISIPFCLAYTLTALLGNCTLLITQADAAHBPVPLAMLAII 71
QY 73 DILISTSSMRMLAIFPNSTTIOFDACLOIPAIHLSGMSVYLLAMAFDRVVAICHP 132
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DB 132 LRHATVTLTLPRTKIGVAAVVRGAALMAPLPVFIKQDPFGSNLSHSYCLHODVMKLAC 191
QY 193 DDIRVNVVYGLVYIISAGLSLISFSYLLIKTVLGL-TREAQAKAFGTCVSHVCAV 251
DB 192 GDTSFNNIYGVAAVMPVIVLDELIVLSYIFILQAVVLLASQEAHYKAFGTCVSHVCAV 251
QY 252 IFYVPGISGMWRHRSKRDSPLPVILANITYLVLPPLANIVGVTKKEIRGRLRLP 309
DB 252 AFYTVVIVSSVWRHVAHAAAPHVHILANFYLLPVPVNPVITVGVTKQIRESLIGVF 309

RESULT 6
US-10-055-877-335
Sequence 335, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchenev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Kaceli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zerhusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eissen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shimkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernel, Corine

APPLICANT: INCYTE GENOMICS, INC.
 APPLICANT: LAL, Preeti
 APPLICANT: TANG, Y. Tom
 APPLICANT: PATTERSON, Chandra
 APPLICANT: YAO, Monique G.
 APPLICANT: SMITH, Leo L.
 APPLICANT: TRIBOULET, Catherine
 APPLICANT: LU, Dying Alina M.
 APPLICANT: YUE, Henry
 APPLICANT: KEAN, Farrah A.
 APPLICANT: POLICKY, Jennifer L.
 APPLICANT: AU-YOUNG, Janice
 APPLICANT: YANG, Junming
 APPLICANT: HARLAND, Lee
 APPLICANT: WALSH, Roderick T.
 APPLICANT: LO, Terence P.
 APPLICANT: BOROMSKY, Mark L.
 TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
 FILE REFERENCE: PI-0044 PCT
 CURRENT APPLICATION NUMBER: US/11/190,188
 CURRENT FILING DATE: 2005-07-27
 PRIOR APPLICATION NUMBER: US/10/220,382
 PRIOR FILING DATE: 2001-03-01
 PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
 PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: PERL Program
 SEQ ID NO 10
 LENGTH: 311
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 7472364CD1
 US-11-190-188-10

Query Match 47.5%; Score 771; DB 7; Length 311;
 Best Local Similarity 47.3%; Pred. No. 3,Je-63;
 Matches 140; Conservative 71; Mismatches 83; Indels 2; Gaps 2.

QY 15 FILTGLGLEBBAQFWLAPPLCSLYLIVLGNLTIIYVRETSHEBMYIFLCMLSGIDI 74
 DB 14 FLPIGLGLDDEHMMWISGPCSVYLVALLGNATLLIVKYEQTLREMFYFLATLSTDL 73
 QY 75 LISTSSPKMLAIFWNSSTTIQPDACLQIPIAHSLSGMESTVLLANAFDRIYAIQPLR 134
 DB 74 ALSTATSPRMIGJFWFPAHREINYGACVACQWFLHAFPEMEAEVLLANAFDRIYAIQPLR 133
 QY 135 HATVLTLPRTKIGVAIVVVGALMAAPLPVFIKQLPFCRSNIILSHSYCLHDDWKLACDD 194
 DB 134 YATLLTSLVVGISMCIVIRPVLTLTDMVYIYLPFCQAHIIASHSYCEHMGIALSCGN 193
 QY 195 IRVVVVVGLIIVISAIGLDSLLISFSYLLILKTVLGP-TREDAQAKAGTCVSHVCAVEIF 253
 DB 194 IIRINGIGLGP-VSFPVLNLVLIGISYVYILRAVFRLPSHDAQQLKALSTCGAHVGVICVF 252
 QY 254 YVPPIGLSMWHRFSKRDPPLPYILANIIYLVPPVLANPIYGVCTKTKIRQRIILFP 309
 DB 253 YIPSVFSLTTRFQHQIPGYIHILVNLVLIIPSLNPIIYGVATKQIRERVLVVF 308

RESULT 8
 US-10-055-877-338
 Sequence 338, Application US/10055877
 Publication No. US20050288241A1
 GENERAL INFORMATION:
 APPLICANT: DecisioFaro, Marc
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Miller, Charles
 APPLICANT: Tochernev, Velizar
 APPLICANT: Zhong, Mei
 APPLICANT: Anderson, David
 APPLICANT: Ballinger, Robert

APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zernhusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patturajan, Meera
APPLICANT: Burgees, Catherine
APPLICANT: Eisen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shimkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Verneet, Corine
APPLICANT: Taulpier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 338
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-338
Query Match 46.8%; Score 758.5; DB 6; Length 321;
Best Local Similarity 45.2%; Pred. No. 4.4e-62;
Matches 140; Conservative 73; Mismatches 96; Indels 1; Gaps 1;
QY 1 MMVDPNGESSATYFILLGLPGLBEAQFWLAPPLCSLYLAVLGNLTIIYVTRSHLHE 60
DB 7 MITSVSPSTNSPFLTGFSGMEQOQWPFSPFSISYAVMLTGNCWLIHYITRPSLHQ 66
QY 61 PMYFLPLCLSGDILISTSSMPKMLAIFWPNSTTIQFPAQLQIFAHISLSGMESTVLLA 120
DB 67 FMFYFLSLMALATLDCMGLSTYYTIVGILMIRIIRISLDSCTAQSYPFHGSLFMESVLLT 126
QY 121 MAPRYVAICHLRHAATVLTLPVTKIGVAANVRGAALMAPLPVPIKQLPFCRSNIISHS 180
DB 127 MAPRYVAICHLRHAATVLTLPVTKIGVAANVRGAALMAPLPVPIKQLPFCRSNIISHS 186
QY 181 YCLHQDVWKLACDDIRVVVYGLVIVISAIGDLSLISFSYLLIKTVLGL-TREAQKA 239

DB 187 FCLHQDLRLACSDIRENSYVALMLVICILLDAIILFISYLLILKSVLVAQSGBRHKL 246
QY 240 FGTGVSHVCAVFIIFYVPIFGLSWHRPSKRRDSPLPVILANIYLLVPVLPNIYGVYKTK 299
DB 247 FGTCTSHICAVLFIYIISLTIMWRKGLSPVAHVIGNIYILFPLMNPITISYKTKQ 306
QY 300 EIRORILRLP 309
DB 307 QIHTRMLRLP 316
RESULT 9
US-11-190-188-9
Sequence 9, Application US/11190188
Publication No. US2006003533A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Chandra
APPLICANT: YAO, Monique G.
APPLICANT: SMITH, Leo L.
APPLICANT: TRIBOULET, Catherine
APPLICANT: LU, Dzung Alma M.
APPLICANT: YUE, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: YANG, Junming
APPLICANT: HARLAND, Lee
APPLICANT: WALSH, Roderrick T.
APPLICANT: LO, Terence P.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0044 PCT
CURRENT APPLICATION NUMBER: US/11/190,188
CURRENT FILING DATE: 2005-07-27
PRIOR APPLICATION NUMBER: US/10/220,382
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 9
LENGTH: 356
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7472363CD1
US-11-190-188-9
Query Match 45.7%; Score 742; DB 7; Length 356;
Best Local Similarity 46.7%; Pred. No. 1.6e-60;
Matches 135; Conservative 70; Mismatches 82; Indels 2; Gaps 2;
QY 22 GLBEAQFWLAPPLCSLYLAVLGNLTIIYVTRSHLHEPMYFLPCLMSGIDILISTSSM 81
DB 66 GLEDFPMHISGPFCSVTLVVALISGNATILLVYKQETLRREMFYTLALISTDLALSAITSV 125
QY 82 PKMLAIFWPNSTTIQFPAQLQIFAHISLSGMESTVLLAAMPDRYVAICHLRHAATVLT 141
DB 126 PMYFLPLCLSGDILISTSSMPKMLAIFWPNSTTIQFPAQLQIFAHISLSGMESTVLLA 185
QY 142 PMYFLPLCLSGDILISTSSMPKMLAIFWPNSTTIQFPAQLQIFAHISLSGMESTVLLA 201
DB 186 LVLVIGISMCIYIRVLLTLPMVYLIYRLPQQAIIIAHSYCEHNGIAKLSGNTIRINGTY 245
QY 202 GLIYIVISAIGDLSLISFSYLLIKTVLGL-TREAQKAGTCVSHVCAVFIIFYVPIGL 260
DB 246 GLFY-VSFPVLTNLVLIGISTYIIRAVFRLPSHQAOLKALSTGCARHGVICVFIIPSVFS 304
QY 261 SMVHRFSKRRDSPLPVILANIYLLVPVLPNIYGVYKTKIRORILRLP 309

Db 305 FULTRFEGHQIPGYHIVANMLYIFPSLNFPIYGVATKQIREVLYVF 353

RESULT 10

US-11-124-367A-496
; Sequence 496, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CU001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-496

Query Match 45.5%; Score 737.5; DB 7; Length 312;
Best Local Similarity 44.4%; Pred. No. 3.6e-60;

Matches 133; Conservative 72; Mismatches 96; Indels 1; Gaps 1;

QY 7 GNESSATYFLILGPGLEBAQFWLAPLCSLYLAVLGNLTIIYVTRHSLHEPMYIFL 66
DB 2 GLNKSASTFQLTGPGKREKAKHWHIFPLLAAYISILGSGTLFLINDNHLHEPMYIFL 61
QY 67 CMISGIDILISTSSMPKMLAIFWNSSTTIQPDACLLQIFAIHSISGNESTVLLAMAFDRY 126
DB 62 AMLAATDGLVLTMPVTLGVLMDHREIGHGACFSQAYFIHTLSVNESGVLLAMAYDCF 121
QY 127 VAICHPLEHATVLTLPRTKIGVAAVVRGALMAP-LPVFIKQLPFCRSNLSHCYCHQ 186
DB 122 ITTHNPKRTYSILNTWVMKIGRAVLTFRAGISLMPYIVRLHWPYCSHVLSHAFCLHQ 181
QY 187 VMKLACDDIRVNVVYGLIYIISAIGLDSLISFSYLLIKTVLGL-TREAQAKAFGTCVS 245
DB 182 VITLACADITFNLPLPVVLPFAMVLDPLFIIFPYIILIKTVWGISGGBRAKALNTCVS 241
QY 246 HVCANVFIFYPFPGLSMVRHRSKRDSPLVYILANLYLVPVLANPIYGVKTEIKRQRI 305
DB 242 HICCLVFFYTVVCLTFIRHFGKIVPVVHITMSYIHFLPPFNNPIYSIKTKQIOSGI 301
QY 306 LRLP 309
DB 302 LRLP 305

RESULT 11

US-11-124-367A-514
; Sequence 514, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CU001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07

; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 514
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-514

Query Match 45.4%; Score 736.5; DB 7; Length 312;
Best Local Similarity 45.8%; Pred. No. 4.4e-60;

Matches 142; Conservative 68; Mismatches 93; Indels 7; Gaps 4;

QY 8 NNESSATYFLILGPGLEBAQFWLAPLCSLYLAVLGNLTIIYVTRHSLHEPMYIFLC 67
DB 3 SSSSHRPFLLTGPGLEBAHWHISVFLPMYISILFNGTLILLIKEDNHLHEPMYIFLA 62
QY 68 MUGIDILISTSSMPKMLAIFWNSSTTIQPDACLLQIFAIHSISGNESTVLLAMAFDRY 127
DB 63 MLAATDGLVLTMPVTLGVLMDHREIGHGACFSQAYFIHTLSVNESGVLLAMAYDRFI 122
QY 128 AICHPLEHATVLTLPRTKIGVAAVVRGALMAP-LPVFIKQLPFCRSNLSHCYCHQ 185
DB 123 AICNPLRTYSILNTWVMKIGRAVLTFRAGISLMPYIVRLHWPYCSHVLSHAFCLHQ 180
QY 186 DVKLACDDIRVNVVYGLIYIISAIGLDSLISFSYLLIKTVLGL-TREAQAKAFGTCV 244
DB 181 DVTKLACADITFNLPLPVVLPFAMVLDPLFIIFPYIILIKTVLSISREBRALNTCV 240
QY 245 SHVCANVFIFYPFPGLSMVRHRSKRDSPLVYILANLYLVPVLANPIYGVKTEIKRQRI 304
DB 241 SHICCVLFFYTVVCLTFIRHFGKIVPVVHITMSYIHFLPPFNNPIYSIKTKQIOSA 300
QY 305 LRLP 314
DB 301 LRLP-TTH 308

RESULT 12

US-10-055-877-123
; Sequence 123, Application US/10055877
; Publication No. US2005028241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchermey, Velizar
; APPLICANT: Zhong, Wei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kerkuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Verne, Corine
; APPLICANT: Raupler Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li


```

; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eileen, Andrew
; APPLICANT: Molenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Verneet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Caeman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 222
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-055-877-222

Query Match      29.3%; Score 475; DB 6; Length 318;
Best Local Similarity 35.7%; Pred. No. 3.8e-36;
Matches 114; Conservative 62; Mismatches 121; Indels 22; Gaps 7;

QY 8 NESSATVPILGL---PGLERAOFWLAPPLCSLYLAVLGNLTLTIYVIRTHSHLEPYI 64
DB 5 NQITVTEVVLGLSHAPKLEKTFVL--ILSMYVILGNGVLVLSILSHLHTEPYF 61
QY 65 FLCLMSGIDILISTSSMEKMLAIFWNSSTTIQFDACLQIFAIHSLSGMESTVLLAMAFD 124
DB 62 FLGLSLFDLCITTSVPLVDGFLTPRKTISSFSCANQWFLSPFMGATECVLLGMMAFD 121
QY 125 RYVAICHPRLRATVLTLEPRVTKIGYAAVVRGALAMAPLVPRIKQLPFGRSNILSHSYCLH 184
DB 122 RYVAICHPRLRATVLTLEPRVTKIGYAAVVRGALAMAPLVPRIKQLPFGRSNILSHSYCLH 181
QY 185 QDWKLCACDDIRVAVVYVGLIYISAGLSLISFVYLLIKTVLGL-TREAOKAPGTC 243
DB 182 LAVKLACADISINVISMGVANVIFLGVPLFIYVSYIFLSTIKRIPSAGRKKAFTC 241
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QY 244 VSHVCAVFIFYVPYPIGLSMVHFPKRDSPULV-----ILANTYLLVPPVLPNPIYVG 295
DB 242 SAHLTVVIFPGTIL---FMWGKPKSKD-PLGADKQDLADLISLFGTLRPMNPIIYS 297
QY 296 VKTKRIRORILRLPHVATH 314
DB 298 LRNDQVKAAYVNL---ASH 313

RESULT 17
US-10-055-877-326
; Sequence 326, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eileen, Andrew
; APPLICANT: Molenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Verneet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Caeman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 326
; LENGTH: 318
; TYPE: PRT
```


ORGANISM: Mus musculus
US-10-055-877-326

Query Match 29.3%; Score 475; DB 6; Length 318;
Best Local Similarity 35.7%; Pred. No. 3.8e-36;
Matches 114; Conservative 62; Mismatches 121; Indels 22; Gaps 7;

QY 8 NESBATTFLIGL---PGLBBAQFWLAPLCSLYLAVGNLTIIYVTRSHLHEPMYI 64
DB 5 NQTVTFEVLIGLSAHPLEKTEPFVL---ILSMVLVILGNGVILVLSIDSLHATPMYF 61
QY 65 FLCLMSGIDILISTSSMPKMLAIFWNSSTTIOFDACLTQIFAIHSLSGMESTVLLAMAF 124
DB 62 FLGLSLFDLCITTSVPLVLDGFLTRKTIISFGCAVOMLSAMGATGCVLLGMMAFD 121
QY 125 RYVAICPLRHATVLTLPVTKIGVAAVVRGALMAPLPVFIKQLPFCRSNLSHSCYCLH 184
DB 122 RYVAICPLRHATVLTLPVTKIGVAAVVRGALMAPLPVFIKQLPFCRSNLSHSCYCLH 181
QY 185 QDVWKLACDDIRVVNVVGLIVTISAGLDSLLISPSYLLIKTVLGL-TREAQAKAFGC 243
DB 182 LAVLKACADISIVISMGVANVIFLGVPVLFIFVSYIFILSTILRIPSAEGRKAFSTC 241
QY 244 VSHVCAVEIFVFPFGLSMVHRFSKRDSPLEV-----ILANITVLVPEVLPVLPVYG 295
DB 242 SAHLTVVITIVYGTIL---FMVGKPKSD-PLGADKODLADGLISLFGLTPLMLNPITIS 297
QY 296 VKTEIRORILRLPHVATH 314
DB 298 LRNDVKAAVRNL---ASH 313

RESULT 18
US-10-055-877-224
Sequence 224, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decistofaro, Marc
APPLICANT: Padigaru, Murailidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mel
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Rattelli, Luca
APPLICANT: Kekuda, Rameesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zernuuen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eileen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkels, Richard
APPLICANT: Gueev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Caeman, Stacie
APPLICANT: Boldog, Ferenc
TITLE OR INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055.877
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598

PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 224
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-224

Query Match 28.6%; Score 464; DB 6; Length 319;
Best Local Similarity 35.3%; Pred. No. 3.8e-35;
Matches 113; Conservative 64; Mismatches 111; Indels 32; Gaps 9;

QY 8 NESBATTFLIGL---PGLBBAQFWLAPLCSLYLAVGNLTIIYVTRSHLHEPMYI 63
DB 5 NETSPVMGFVLLRASHAPLEKTEPFVL---ILMTVLVILGNGVILVLTSLDLSLHATPMY 61
QY 64 IFCLMSGIDILISTSSMPKMLAIFWNSSTTIOFDACLTQIFAIHSLSGMESTVLLAMAF 123
DB 62 FLGLSLFDLCITTSVPLVLDGFLTRKTIISFGCAVOMLSAMGATGCVLLGMMAFD 121
QY 124 DRYVAICPLRHATVLTLPVTKIGVAA-VVRGALMAPLPVFIKQLPFCRSNLSHSCYCLH 182
DB 122 DRYVAICPLRHATVLTLPVTKIGVAA-VVRGALMAPLPVFIKQLPFCRSNLSHSCYCLH 180
QY 183 LHQVWKLACDDIRVVNVVGLIVTISAGLDSLLISPSYLLIKTVLGL-TREAQAKAFGC 241
DB 181 EILAVLKACADISIVISMGVANVIFLGVPVLFIFVSYIFILSTILRIPSAEGRKAFSTC 240
QY 242 TCVSHVCAVEIFVFPFGLSMVHRFSKRDSPLEV-----PLPVITIANITVLVPEV 288
DB 241 TCSAHLTVVITIVYGTIL---LFMVGKPKSDSGADKEDLSDKLPL-----FVGVTWPM 291
QY 289 LNPVYGVKTEIRORILRL 308
DB 292 LNPVYGVKTEIRORILRL 311

RESULT 19
US-11-190-188-12
Sequence 12, Application US/11190188
Publication No. US20060035331A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Chandra
APPLICANT: YAO, Monique G.
APPLICANT: SHIH, Leo L.
APPLICANT: TRIBOULEY, Catherine
APPLICANT: LU, Dzung Aina M.
APPLICANT: YOS, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: YANG, Junning

```
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROMSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/11/190,188
; PRIOR FILING DATE: 2005-07-27
; PRIOR APPLICATION NUMBER: US/10/220,382
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 7472435CD1
US-11-190-188-12
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Query Match 28.6%; Score 464; DB 7; Length 319;
Best Local Similarity 35.3%; Pred. No. 3.8e-35;
Matches 113; Conservative 64; Mismatches 111; Indels 32; Gaps 9;
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QY 8 NNESSATYFLLIGLPGLEBAQFWLAFPLCSLYLVIAVGNLTIIYVTRTHSLHEPMY 63
DB 5 NESTVWGFVLFPSMFPAHNRGGLFPIPLLLIYGFILGNLIMFVIQVGNALHTPLXFF 61
QY 64 IFLCMLSGIDILISTSMRPMKLAIFWPNSTTIQFDACLQIFAIHSLSGMESTVLLAMAF 123
DB 62 FFLGNLSTLDCFTTSVPLVLDSELTPOETISFSAQVQMALSPAMAGTECLLSMNAF 121
QY 124 DRYVAICHPLRHATVLTLPRTVKIGVAA-VVRGALMLAPLPVFIQQLPFCRSNLSHSYC 182
DB 122 DRYVAICHPLRYSVISMKAAYMPMASSWALGGAASVHTSLAI-QLPFCGDNVNHFTC 180
QY 183 LHQVWMLACDDIRVVNVVYGLIVISAIGLDSLISFYLILKTVLG-TREAQAKAFG 241
DB 181 EILAVLKACADISINVISMETVNIPLGVPLVPLISFVITITILIPSAEGRKXVFS 240
QY 242 TCVSHVCAVFIIFYVFFIGLSMVHRSKRDS-----PLPYILANIYLLVPPV 288
DB 241 TCSAHLTVVIVFYGR--LFFVYGGKPKGKDSWGADKEDLSDKLPL-----FYGVVTPM 291
QY 289 LNPVYGVKTEIKRRIIRL 308
DB 292 LNPVIYSLRNDVKAAYRRL 311
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RESULT 20
US-10-511-538-21

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; Sequence 21, Application US/10511538
; Publication No. US20060026700A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
; FILE REFERENCE: 16U 200 PCT
; CURRENT APPLICATION NUMBER: US/10/511,538
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: US 60/372,669
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,882
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/424,336
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/374,823
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/376,558
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 60/381,366
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; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/403,648
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-538-21
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Query Match 28.5%; Score 463; DB 6; Length 319;
Best Local Similarity 33.5%; Pred. No. 4.7e-35;
Matches 106; Conservative 63; Mismatches 133; Indels 14; Gaps 5;
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QY 6 NNESSATYFLLIGLPGLEBAQFWLAFPLCSLYLVIAVGNLTIIYVTRTHSLHEPMYIF 65
DB 7 SGNQVWTFVLFPSMFPAHNRGGLFPIPLLLIYGFILGNLIMFVIQVGNALHTPLXFF 66
QY 66 IFLCMLSGIDILISTSMRPMKLAIFWPNSTTIQFDACLQIFAIHSLSGMESTVLLAMAFDR 125
DB 67 ISVSLFLEICVTTTIPRMUSCLISEQKISVAGCLQWTFHSLGITESCVLTMAIDR 126
QY 126 YVAICHPLRHATVLTLPRTVKIGVAAVVRGALMLAPLPVFIQQLPFCRSNLSHSYCLHQ 185
DB 127 YVAICNPLRYPITIMIPKLCIQLTGSCFCGFLVLPRIAWISTLPFGSGNQIHQIFCDFT 186
QY 186 DVMKLAGDDIRVVNVVYGLIVISAIGLDSLISF-----SYLILKTVLG-TREAQAKA 239
DB 187 PVLSLACTDT-----FLVAVVDVIAHNAEIVASVLVLTALSTIRITIIYLGMSHSGHNKA 240
QY 240 FGTCVSHVCAVFIIFYVFFIGLSMVHRSKRDSPLPYILANIYLLVPPVNPVYGVKTK 299
DB 241 FSTQANHL-AVFLLPFSVAN-VYLRFSATVSVFMDRAIVTFLIAPFPNPITISLXNK 298
QY 300 EIRQRIIRLRHVATHA 315
DB 299 DMKEAIRGLRPHYOKRA 314
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Search completed: March 9, 2006, 08:44:24
Job time : 23 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:25:34 ; Search time 40 Seconds
(without alignments)
764.923 Million cell updates/sec

Title: US-10-001-469A-2866

Perfect score: 1622
Sequence: 1 MMWDPNNGESSATYFLLGL.....KRIQRILRLPHYVATNASEP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 80:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552	34.0	292	2 A60547	hypothetical prote
2	473.5	29.2	313	2 E45774	odorant receptor 8
3	453	27.9	307	2 S29710	olfactory receptor
4	440	27.1	312	2 A46247	olfactory receptor
5	434.5	26.8	312	2 I23701	olfactory receptor
6	431.5	26.6	310	2 E23701	olfactory receptor
7	430.5	26.5	319	2 UC5624	olfactory receptor
8	429.5	26.5	312	2 S29708	olfactory receptor
9	428	26.4	328	2 S20572	odorant receptor 2
10	427.5	26.4	314	2 S20572	olfactory receptor
11	425.5	26.2	314	2 A37286	olfactory receptor
12	423.5	26.1	314	2 S29707	olfactory receptor
13	420.5	25.9	321	2 H45774	odorant receptor 3
14	418.5	25.8	305	2 S29711	olfactory factor 0
15	418.5	25.8	309	1 S51356	olfactory receptor
16	413	25.5	312	2 A48413	probable olfactory
17	411	25.3	160	2 S58066	probable olfactory
18	411	25.3	344	2 I45774	odorant receptor 1
19	407.5	25.1	311	2 UC5200	chemoreceptor 1B33
20	407	25.1	313	2 S20571	olfactory receptor
21	404.5	24.9	312	2 G23701	olfactory receptor
22	404.5	24.9	313	2 B23701	olfactory receptor
23	402.5	24.8	311	2 H23701	olfactory receptor
24	402.5	24.8	314	2 H23701	olfactory receptor
25	401	24.7	317	2 F45774	odorant receptor 4
26	396.5	24.4	316	2 A57069	olfactory receptor
27	395.5	24.4	328	2 D45774	odorant receptor 3
28	395.5	24.4	328	2 A45774	odorant receptor 3
29	393.5	24.3	328	2 B45774	odorant receptor 3

30	390.5	24.1	320	2 S20573	olfactory receptor
31	388.5	24.0	312	2 A46750	olfactory receptor
32	386.5	23.8	304	2 S29709	olfactory receptor
33	384.5	23.7	315	2 UC5836	olfactory receptor
34	383.5	23.6	328	2 C45774	odorant receptor 3
35	383	23.6	333	2 A23701	olfactory receptor
36	379.5	23.4	327	2 F23701	olfactory receptor
37	375	23.1	317	2 D23701	olfactory receptor
38	371.5	22.9	315	2 UC4658	olfactory receptor
39	370	22.8	315	2 UC5201	chemoreceptor 1B56
40	366	22.6	318	2 UC5202	chemoreceptor 1B64
41	313.5	19.3	234	2 S29000	G protein-coupled
42	310.5	19.1	222	2 S29001	odorant receptor (
43	303.5	18.7	264	2 PC4369	olfactory receptor
44	289.5	17.8	234	2 S28939	G protein-coupled
45	285.5	17.6	222	2 D40745	odorant receptor (
46	280.5	17.3	234	2 S28938	G protein-coupled
47	277	17.1	225	2 I38478	olfactory receptor
48	261.5	16.1	232	2 S29001	G protein-coupled
49	259.5	16.0	216	2 I38474	olfactory receptor
50	254.5	15.7	216	2 I38470	olfactory receptor
51	254.5	15.7	216	2 I38480	olfactory receptor
52	249.5	15.4	216	2 I38479	olfactory receptor
53	239.5	14.8	222	2 C40745	odorant receptor (
54	235.5	14.5	135	2 PN0530	G protein-coupled
55	232.5	14.3	216	2 I38472	olfactory receptor
56	232.5	14.3	216	2 I38464	olfactory receptor
57	227.5	14.0	185	2 S28936	G protein-coupled
58	226	13.8	215	2 I38473	olfactory receptor
59	223.5	13.8	216	2 I38482	olfactory receptor
60	221.5	13.7	216	2 I38483	olfactory receptor
61	220.5	13.6	216	2 I38476	olfactory receptor
62	216.5	13.3	216	2 I38461	olfactory receptor
63	212.5	13.1	216	2 I38477	olfactory receptor
64	211.5	13.0	168	2 S28937	G protein-coupled
65	210.5	13.0	163	2 S58028	probable olfactory
66	194.5	12.0	157	2 S58000	probable olfactory
67	187.5	11.6	332	2 A57055	melanocortin recep
68	187	11.5	320	2 S17177	probable G protein
69	184.5	11.4	318	2 S38511	adenosine receptor
70	182.5	11.3	352	2 JB0296	thyrotropin releas
71	182	11.2	143	2 S58006	probable olfactory
72	181.5	11.2	161	2 A40745	odorant receptor (
73	181.5	11.2	317	2 S29204	melanotropin recep
74	181	11.2	165	2 I38471	olfactory receptor
75	180	11.1	320	2 A46152	A3 adenosine recep
76	180	11.1	323	2 S43850	melanocortin 3 rec
77	178	11.0	143	2 S58071	probable olfactory
78	177	10.9	154	2 S58069	probable olfactory
79	176.5	10.9	317	2 S45708	MGR receptor - bov
80	176	10.9	325	2 UN0764	melanocortin recep
81	174.5	10.8	157	2 S58068	probable olfactory
82	174	10.7	325	2 UC5592	melanocortin 5 rec
83	173.5	10.7	584	2 JC7809	bulfinthin recepto
84	173	10.7	427	2 S50150	Gastric CCK-A rece
85	172.5	10.6	157	2 S58033	probable olfactory
86	172.5	10.6	360	2 B46647	melanocortin recep
87	172	10.6	314	2 S71420	melanocortin 1 rec
88	171	10.6	314	2 S71420	melanocortin 1 rec
89	170.5	10.5	157	2 S58019	probable olfactory
90	169.5	10.5	337	2 S68678	adenosine receptor
91	169	10.4	324	2 S55302	A(1) adenosine rec
92	168.5	10.4	157	2 S57939	probable olfactory
93	168.5	10.4	157	2 S58035	probable olfactory
94	168	10.4	325	2 UC2193	melanocortin recep
95	167.5	10.3	157	2 S58026	probable olfactory
96	167.5	10.3	158	2 S58016	probable olfactory
97	167	10.3	362	2 JC0694	angiotensin II rec
98	166.5	10.3	157	2 S58023	probable olfactory
99	164.5	10.1	156	2 S58072	probable olfactory
100	164.5	10.1	157	2 S58030	probable olfactory

ALIGNMENTS

RESULT 1

A60547

hypothetical protein (HPRH breakpoint 3' region) - human (fragment)

N:Alternate names: olfactory receptor homolog

C:Species: Homo sapiens (man)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999

C/Accession: A60547; A60482

R:Feingold, E.A.; Forget, B.G.

Blood 74, 2178-2186, 1989

A>Title: The breakpoint of a large deletion causing hereditary persistence of fetal hem

A:Reference number: A60547; MUID:90028751; PMID:2478223

A:Accession: A60547

A:Molecule type: DNA

A:Residues: 1-292 <FEI>

A:Cross-references: UNIPARC:UPI0000178388

C:Superfamily: olfactory receptor OR14

Query Match 34.0%; Score 552; DB 2; Length 292;

Best Local Similarity 40.3%; Pred. No. 1.8e-40;

Matches 114; Conservative 49; Mismatches 88; Indels 32; Gaps 6;

QY 17 LIGPGLBEAQFWLAFPLCSLYLAVLGNLTIIYVREHSLHEPMYIFLCMLSGIDILI 76

DB 29 LVGIPGLSEVQCMGIPFCATYILAMIGNSLSTIKERSLHEFLYIFLCMLGATDIAL 88

QY 77 STSGMPKMLAIFWPNSTTIQPDACILQIF-----AIH-SLSGSESTVLLAMADRYVAI 129

DB 89 ASSIMPKMLGYSGL-----MCLKSILIPACEFNVVPHIAGIESGILVAMALDRYVAI 140

QY 130 CHPRHATVTLPRVTIKIGVAAYVGAALMAPLPVFIR-QLPFGCSNLSHCYLDQVM 188

DB 141 CYPHATVTLPRVTIKIGVAAYVGAALMAPLPVFIR-QLPFGCSNLSHCYLDQVM 200

QY 189 KLACDDIRVNVVGLIVISAIGDSLISFSYLLIKTVLGL-TREAQAKAFGTGVSHV 247

DB 201 KLAANAVQNKITIGLFFVAAGPDLFTITSLYIGIFITVTRLPCKEAPFAFNCIAHI 260

QY 248 CAVFTIYVPFVIGLSMVRHFRSKRDSPLFVILANIYLVPPVLN 290

DB 261 CVFLQFYLALFFSFPTHRFGSH-----IPPYIH 288

RESULT 2

E45774

odorant receptor 8 - channel catfish

C/Species: Ictalurus punctatus (channel catfish)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: E45774

R:Ngel, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

Cell 72, 657-666, 1993

A>Title: The family of genes encoding odorant receptors in the channel catfish.

A:Reference number: A45774; MUID:93201590; PMID:791654

A:Accession: E45774

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-313 <NGA>

A:Cross-references: UNIPROT:Q9PSJ5; UNIPARC:UPI0000042025

A:Experimental source: olfactory epithelium

A>Note: sequence extracted from NCBI backbone (NCBIP:127748)

C:Superfamily: olfactory receptor OR14

C:Keywords: olfaction; transmembrane protein

Query Match 29.2%; Score 473.5; DB 2; Length 313;

Best Local Similarity 34.1%; Pred. No. 1.2e-33;

Matches 105; Conservative 66; Mismatches 132; Indels 5; Gaps 4;

QY 2 MVDPRGNSSATYFTLIGLPGLEAQFWLAFPLCSLYLAVLGNLTIIYVREHSLHEP 61

DB 1 MLAPVQNISFTT-FTLTGFHDGEGPILSIPLYLMLFSLSTSNLTIIYLIISQRLASP 59

QY 62 MYFLCMLSGIDILISTSMKMLAIFWPNSTTIQPDACILQIFAIHSLSGMESTVLLAM 121

DB 60 MCLILGMNAVVDLSMPFCFPMNLSTLFNMKGSLVGLCVQMCHACAGFGSTILLMM 119

QY 122 AFDRYVAICHPLRHATVTLPRVTIKIGVAAYVGAALMAPLPVFIR-KQLPFRSNILSHSY 181

DB 120 ALDRFPAICBPLVYQKTMGMENFLKFIIPVIRMLPFIITIVSWAGKLTFCETIEIDHCV 179

QY 182 CLHODVWKLACDDIRVNVVGLIVISAIGDSLISFSYLLIKTVLGLTRBAQAKAFG 241

DB 180 CERNALVQLACGDISINNALGLTVPLTIDPFITISIVIVLSIL-RSGKACLAAYN 238

QY 242 TCVSHVCAVFIFYVPFVIGLSMVRHFRSKRDSPLF-VILANIYLVPPVLNPIYGVKIKE 300

DB 239 TCIHIITVMSLSLFPALIAFLSYRI--RNPSPSRVFLSTWYLPFGCFNPIIYGVRIKE 296

QY 301 IRQRILRL 308

DB 297 IREQFLKL 304

RESULT 3

S29710

olfactory receptor OR18 - rat

C/Species: Rattus norvegicus (Norway rat)

C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998

C/Accession: S29710

R:Ramang, K.; Krieger, J.; Strotmann, J.; Bookhoff, I.; Kludick, S.; Baumstark, C.; Breer, N.

Nature 361, 353-356, 1993

A>Title: Cloning and expression of odorant receptors.

A:Reference number: S29707; MUID:93149273; PMID:7678922

A:Accession: S29710

A:Molecule type: mRNA

A:Residues: 1-307 <RAM>

A:Cross-references: UNIPARC:UPI000004187C

C:Superfamily: olfactory receptor OR14

Query Match 27.9%; Score 453; DB 2; Length 307;

Best Local Similarity 33.6%; Pred. No. 7.3e-32;

Matches 107; Conservative 64; Mismatches 125; Indels 22; Gaps 7;

QY 7 GNSSATYFTIIGL---PGLBEAQFWLAFPLCSLYLAVLGNLTIIYVREHSLHEPMY 63

DB 2 GENNITTEFTLGLTQDPDGRKALFVIFP---LIYIVTMGNLIVVIVASPSISGPMY 58

QY 64 IFLCMLSGIDILISTSMKMLAIFWPNSTTIQPDACILQIFAIHSLSGMESTVLLAMAF 123

DB 59 FFLASLSLIDLTFSTALSPKLIADLYDQKTSFRACKSQLFIEHLRGVDIVILVAMAY 118

QY 124 DRYVAICHPLRHATVTLPRVTIKIGVAAYVGAALMAPLPVFIRKQLPFCRGNILSHSYCL 183

DB 119 DRYVAICHPLRHATVTLPRVTIKIGVAAYVGAALMAPLPVFIRKQLPFCRGNILSHSYCL 178

QY 184 HQDVWKLACDDIRVNVVGLIVI---ISAIGDSLISFSYLLIKTVLGLTRBAQAKA 239

DB 179 MSPLVIACTD---TYFGLTVIANGVNCIVIFITLLG-SYGLIISLTKQSOEGGRKA 234

QY 240 FGTCVSHVCAVFIFYVP-FIGLSMVRHFRSKRDSPLFVILANIYLVPPVLNPIYGVK 297

DB 235 LSTSSHLLVILFPVCFITFMAYPVNF-----PIDKCIYFTVYITTPMLNPLIYLR 288

QY 298 TKEIRORILRLFHVATTA 315

DB 289 NSRIKSKCKKLMCMQMLHA 306

RESULT 4

A46247

olfactory receptor OR3 - mouse

C/Species: Mus musculus (house mouse)

C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A46247

R:Nef, P.; Hermans-Borgmeyer, I.; Artlerer-Plin, H.; Beasley, L.; Dönne, V.E.; Heinemann,

RESULT 10
S20572
Olfactory receptor - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S20572
R/Parmentier, M.; Libert, F.; Schuurmans, S.; Schliffmann, S.; Lefort, A.; Eggerickx, D.;
Nature 355, 453-455, 1992
A/Title: Expression of members of the putative olfactory receptor gene family in mammals
A/Reference number: S20571; MUID:92131132; PMID:1370859
A/Accession: S20572
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-314 <P&R>
A/Cross-references: UNIPROT:P30953; UNIPARC:UPI0000041BB6; EMBL:X64994; NID:g32085; PIDN:
C/Superfamily: olfactory receptor OR14
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.4%; Score 427.5; DB 2; Length 314;
Best Local Similarity 34.5%; Pred. No. 1.2e-29;
Matches 108; Conservative 64; Mismatches 120; Indels 21; Gaps 8;

QY 8 NESGATYFIIIGLPGLEBAQ--FWLAFPLCSLYLAVGNLTIIYVTRHSHLHEPMYIFLC 67
DB 5 NQTVISQFLLFLPISEHQHVFYALF--LSWYLTVLVGNLIIIIIIHLDSHLTPMYLF 64
QY 68 MLGSGIDILISTSSMPKMLAIFWNSSTTIQPDACLIQIFAHLSGMSSTVLLAMAAPDRYV 127
DB 65 NLSPSDLCFSSVTPKLLQNNQNDPSIPYADCTQWYFLLFGDLSFLVMAAYDRYV 124
QY 128 AICPPLHATYVTLPRYTKGV--AVRGALMAPLPVFIKQLPFCRSNLSHSYCLH 184
DB 125 AICPPL-HYTKIMSPMLCLAVALSWSVLTTFHAMLT--LMARLCFCADNVIPHFCDM 181
QY 185 QDVWKLACDDIRVN----VYGLIIVIIISAIGLSLISFSYLLIKTVLGL-TRBAQAK 238
DB 182 SALKMLAFSDIRVBEWYIFPIGSLIVT----PPLLSGVARIIVSILKVPSSKIGCK 236
QY 239 AFGTGVSHVCAVFIYVPFIGLSMVHRFSKRDSPL-PVILANIYLLVPPVLANPIYGVK 297
DB 237 AFSCTGSHLSVSLFYGVTVGLYLC--SSANSTLMDTQWAMMYTVTTPMLNPFITSLR 293
QY 298 TKETIRQRIILRL 310
DB 294 NRDMKGLSRVTH 306

RESULT 11
A37286
Olfactory receptor 115 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C/Accession: A37286
R/Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A/Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A/Reference number: A23701; MUID:91191556; PMID:1840504
A/Accession: A37286
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-314 <BUC>
A/Cross-references: UNIPROT:P23274; UNIPARC:UPI0000040A93; GB:M64392; NID:g205845; PIDN:
C/Superfamily: olfactory receptor OR14
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.2%; Score 425.5; DB 2; Length 314;
Best Local Similarity 33.2%; Pred. No. 1.8e-29;
Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;

QY 8 NESGATYFIIIGLPGLEBAQ--FWLAFPLCSLYLAVGNLTIIYVTRHSHLHEPMYIF 65
DB 5 NQTVISQFLLFLPISEHQHVFYALF--LSWYLTVLVGNLIIIIIIHLDSHLTPMYLF 62

DB 5 NQTVISQFLLFLPISEHQHVFYALF--LSWYLTVLVGNLIIIIIIHLDSHLTPMYLF 62
QY 66 LCMISGIDILISTSSMPKMLAIFWNSSTTIQPDACLIQIFAHLSGMSSTVLLAMAAPDR 125
DB 63 LSNLSPSDLCFSSVTPKLLQNNQNDPSIPYAGCLTQWYFLLFGDLSFLVMAAYDR 122
QY 126 YVAILCHPLHATYVTLPRYTKIGVAAYVRGAALM--APL-PVFIKQLPFCRSNLSHSY 181
DB 123 YVAILCHPLHATYVTLPRYTKIGVAAYVRGAALM--APL-PVFIKQLPFCRSNLSHSY 178
QY 182 CLHODVWKLACDDIRVN----VYGLIIVIIISAIGLSLISFSYLLIKTVLGL-TRBA 235
DB 179 CDISPLKLCSDTRHVELVIFWVGGLVYIPV----LIIVYAVVASILKVPSSVGRG 233
QY 236 QAKAFGTGVSHVCAVFIYVPFIGLSMVHRFSKRDSPL-PVILANIYLLVPPVLANPIYVG 295
DB 234 IHKIFSTGSHLSVSLFYGVTVGLYLC--SSANSTVKESTVWAMMYTVTTPMLNPFITSLR 291
QY 296 VKTETIRQRIILRL 308
DB 292 LRNDMKGLSRVTH 304

RESULT 12
S29707
Olfactory receptor OR5 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C/Accession: S29707; B37286
R/Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer,
Nature 361, 353-356, 1993
A/Title: Cloning and expression of odorant receptors.
A/Reference number: S29707; MUID:93149273; PMID:7678922
A/Accession: S29707
A/Molecule type: mRNA
A/Residues: 1-314 <RAM>
A/Cross-references: UNIPROT:Q04059; UNIPARC:UPI0000042031
R/Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A/Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A/Reference number: A23701; MUID:91191556; PMID:1840504
A/Accession: B37286
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 193-236 <BUC>
A/Cross-references: UNIPARC:UPI000008403; GB:M64375; NID:g205811; PIDN:AAA41738.1; PID:
C/Keywords: G protein-coupled receptor; membrane protein

Query Match 26.1%; Score 423.5; DB 2; Length 314;
Best Local Similarity 34.4%; Pred. No. 2.7e-29;
Matches 104; Conservative 64; Mismatches 119; Indels 15; Gaps 7;

QY 8 NESGATYFIIIGLPGLEBAQ--FWLAFPLCSLYLAVGNLTIIYVTRHSHLHEPMYIF 65
DB 5 NQTVISQFLLFLPISEHQHVFYALF--LSWYLTVLVGNLIIIIIIHLDSHLTPMYLF 62
QY 66 LCMISGIDILISTSSMPKMLAIFWNSSTTIQPDACLIQIFAHLSGMSSTVLLAMAAPDR 125
DB 63 LSNLSPSDLCFSSVTPKLLQNNQNDPSIPYAGCLTQWYFLLFGDLSFLVMAAYDR 122
QY 126 YVAILCHPLHATYVTLPRYTKIGVAAYVRGAALM--APL-PVFIKQLPFCRSNLSHSY 181
DB 123 YVAILCHPLHATYVTLPRYTKIGVAAYVRGAALM--APL-PVFIKQLPFCRSNLSHSY 178
QY 182 CLHODVWKLACDDIRVN----VYGLIIVIIISAIGLSLISFSYLLIKTVLGL-TRBAQAKAF 240
DB 179 CDMKALIKLACSDTRHVELVIFWVGGLVYIPV----LIIVYAVVASILKVPSSGIGYKAF 238
QY 241 GTCVSHVCAVFIYVPFIGLSMVHRFSKRDSPL-PVILANIYLLVPPVLANPIYGVTKS 300
DB 239 SSCGSHLSVSLFYGVTVGLYLC--SSANSTVKESTVWAMMYTVTTPMLNPFITSLRND 296
QY 301 IR 302

Db 234 GRKAPC7C5HLMVAVGIFGSGITFMILKXSSNSLSLQEK-----VSSVFYTYVPMNLPL 289

QY 293 VYGVKTKRIRORILR 307

Db 290 IYSLRNKDVKKALGR 304

RESULT 16

A48413

probable olfactory receptor OLFR1 - human

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A48413

R/Schumann, S.; Muscatelli, F.; Miot, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.

Cytogenet. Cell Genet. 63, 200-204, 1993

A/Title: The OLFR1 gene encoding the HGM07B putative olfactory receptor maps to the 17p

A/Reference number: A48413, MUID:93251832; PMID:8097991

A/Accession: A48413

A/Molecule type: DNA

A/Residues: 1-312 <SC>

A/Cross-references: UNIPROT:P34982; UNIPARC:UP10000041806; EMBL:X65857; NID:9425220; PIR

A/Note: sequence extracted from NCBI backbone (NCBIN:131483, NCBIIP:131485)

C/Genetics:

A/Gene: GDB:OLFR1

A/Cross-references: GDB:136274; OMIM:164342

A/Map position: 17p13-17p12

C/Superfamily: olfactory receptor OR14

C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F/26-49/Domain: transmembrane #status predicted <TM1>

F/57-79/Domain: transmembrane #status predicted <TM2>

F/101-120/Domain: transmembrane #status predicted <TM3>

F/140-164/Domain: transmembrane #status predicted <TM4>

F/197-219/Domain: transmembrane #status predicted <TM5>

F/237-255/Domain: transmembrane #status predicted <TM6>

F/272-291/Domain: transmembrane #status predicted <TM7>

F/5/Binding site: carbohydrate (asn) (covalent) #status predicted

F/137,232,290/Binding site: phosphate (Ser) (covalent) #status predicted

F/312/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 25.5%; Score 413; DB 2; Length 312;

Best Local Similarity 30.6%; Pred. No. 2.2e-28;

Matches 97; Conservative 81; Mismatches 107; Indels 32; Gaps 12;

QY 7 GNSSATYFLLIGL---PGLBQAQFMAFLPCLSYLAVLGNLTIIYVTRTHSLHEPMY 63

Db 4 GNOSGESEFLILGSSSEPEQQIIFMW---FLSMYLVTVGVNVLIIAISDSRLHTPVY 60

QY 64 IPICMISGIIILISTSMRPMKALIFWNSITTIOPDACILQIFAHISLGSSESTVLLMAF 123

Db 61 PFLANISFTDLPFYVNTIIPKMLVNLQSHNKAISYAGCLTQLYFLVSLVALDNLITLAVMAY 120

QY 124 DRVVAICHPRLHATVTLPR---VTKIGVAAVVGAALMAPLPVFIKQLPFCRSNLS 178

Db 121 DRVVAICHPRLHATVTLPR---PGLCILLLSLCLWLSVLG---LHHTL---LMTVTPFGSKIH 175

QY 179 HSYCLHODVMKACDDIRVN---VVYGLVIISAIGLDSLISFSYLLIKTVLGLTRE 234

Db 176 YIFCEMVLVLRMCNSIQINHTVLIATGCFILIPFG---FVLIISYVLIIRAILRIPSV 231

QY 235 AQK-KARGTCVSHCAPIFY--VPFGLSMVHFRKRDSPPLVLIANIYLLVPLVLP 291

Db 232 SKKYKASTCASHGASLFLFGTLCMVYLPKRLHTYV-KOSVATV---MTAAVTPPMNP 286

QY 292 IVYGVKTKRIRORILR 308

Db 287 FIYSLRNKDVKKALGR 303

RESULT 17

S58066

probable olfactory receptor tpcr33 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C/Accession: S58066

R/Vanderhaeghen, P.; Schumann, S.; Vassart, G.; Parmentier, M.

Submitted to the EMBL Data Library, July 1995

A/Description: Male germ cells from several mammalian species express a specific reperto

A/Reference number: S57995

A/Accession: S58066

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-160 <VAN>

A/Cross-references: UNIPROT:Q62336; UNIPARC:UP10000042009; EMBL:X89685; NID:9902668; PIR

C/Superfamily: olfactory receptor OR14

Query Match

25.3%; Score 411; DB 2; Length 160;

Best Local Similarity 50.9%; Pred. No. 1.6e-28;

Matches 82; Conservative 29; Mismatches 46; Indels 4; Gaps 3;

QY 129 ICHPLRHATVTLPRVYKIGVAAVVGAALMAPLPVFIKQLPFCRSNI-LSHSYCLHODV 187

Db 1 ISNPLRASYLVLTNNVIRIIOVALTTTATSLPLPLKRLNCPGKILLSHSPCFHADV 60

QY 188 MKLACDDIRVNVYGLVITISAIGLDSLISFSYLLIKTVLGLT---RBAQAKAFGTCVS 245

Db 61 MKLACADITVNIILYGLVYVSTVIGIDSLILVMSYSILHTVMGLASPR-RVRTLNTCVS 119

QY 246 HVCAVPIFYVPIGLSMVHFRKRDSPPLVLIANIYLLVLP 286

Db 120 HISAVLFIYPIVIGSMVHFRKRLPHITVALVAYVLVP 160

RESULT 18

145774

odorant receptor 1 - channel catfish

C/Species: Ictalurus punctatus (channel catfish)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: 145774

R/Neal, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

Cell 72, 657-666, 1993

A/Title: The family of genes encoding odorant receptors in the channel catfish.

A/Reference number: A45774; MUID:93201590; PMID:7916654

A/Accession: 145774

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-344 <NGA>

A/Cross-references: UNIPROT:Q9PSJ1; UNIPARC:UP100000FC739

A/Experimental source: olfactory epithelium

A/Note: sequence extracted from NCBI backbone (NCBIIP:127744)

C/Superfamily: olfactory receptor OR14

C/Keywords: olfaction; transmembrane protein

Query Match 25.3%; Score 411; DB 2; Length 344;

Best Local Similarity 31.7%; Pred. No. 3.7e-28;

Matches 99; Conservative 72; Mismatches 129; Indels 12; Gaps 6;

QY 6 NGNESSATY-----FLILGPGLEBAQFMAFLPCLSYLAVLGNLTIIYVTRTHSLHE 60

Db 6 NALSANATFIRPSTFIYNGFTYNIPIHTKYAF-LCIAVAVTVAGNSITMCTIYLABSLAT 64

QY 61 PMYIFLCMISGIIILISTSMRPMKALIFWNSITTIOPDACILQIFAHISLGSSESTVLLA 120

Db 65 AKITIVNLAISLQSSSALIPKLIDFLFENQYISYBAQANMFVLPFTVQSLTLV 124

QY 121 MADRYVAICHPRLHATVTLPRVYKIGVAAVVGAALMAPLPVFIKQLPFCRSNLSHS 180

Db 125 MAYDRVVALICFPRKYNTVTKEMTLLIVTWFSISILVALVLRSLFSCSVIINSY 184

QY 181 YCLHODVMKACDDIRVN---VVYGLVIISAIGLDSLISFSYLLIKTVLGLTREAO-A 237

Db 185 FCDHGPILLANGDKPIRNMAIGCFVYLDVCFP---LLIIVSYICIGIALMNTSHGERR 242

QY 238 KAFGTCVSHCAVPIFYVPIGLSMVHFRKRDSPPLVLIANIYLLVPLVLPVYGVK 297

Db 243 KAKTCTSHLILVALFYLPIFGTNTSLTSISINAND-RINSLTQLIIPMLNPITVTLK 301

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:22:14 ; Search time 231 Seconds

(Without alignments)
971.247 Million cell updates/sec

Title: US-10-001-469A-2866

Perfect score: 1622

Sequence: 1 MWMDPMGNESATYFILIG.....KEIRQRTLRPHVATASRP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1619	99.8	318	2	061F93_HUMAN
2	1614	99.5	317	1	051B1_HUMAN
3	1614	99.5	317	1	05S4P5_HUMAN
4	1612	99.4	318	2	066X57_HUMAN
5	1512	93.2	317	2	08VG27_MOUSE
6	1498	92.4	317	2	05MD65_RAT
7	1113	68.6	223	2	06SNE2_PPRIM
8	985	60.7	320	2	08VBV9_MOUSE
9	979	60.4	320	1	051E2_HUMAN
10	979	60.4	320	1	061F94_HUMAN
11	977	60.2	320	1	051E2_RAT
12	967.5	59.6	322	2	08VP03_MOUSE
13	937.5	57.8	324	1	051D1_HUMAN
14	914.5	56.4	315	2	08VH05_MOUSE
15	901.5	55.6	312	2	08VH11_MOUSE
16	892.5	55.0	314	1	051G2_HUMAN
17	892.5	55.0	314	1	061F47_HUMAN
18	877	54.1	313	2	08VH17_MOUSE
19	875.5	54.0	314	2	08VG26_MOUSE
20	873.5	53.9	314	2	08VG22_MOUSE
21	873.5	53.9	318	2	08VG23_MOUSE
22	868.5	53.5	312	1	05112_HUMAN
23	868.5	53.2	317	2	061F81_HUMAN
24	862.5	53.2	312	2	08VH01_MOUSE
25	859.5	53.0	319	2	08VH80_MOUSE
26	857.5	52.9	314	2	07TR80_MOUSE
27	857.5	52.9	319	2	08VG28_MOUSE
28	854	52.7	317	2	08VH04_MOUSE
29	852.5	52.6	319	2	09EQ07_MOUSE
30	852	52.5	317	2	08VEX9_MOUSE
31	846.5	52.2	319	2	08VGV9_MOUSE

32	844.5	52.1	314	2	07TR52_MOUSE	07TR52 mus musculus
33	843	52.0	326	2	07TR56_MOUSE	07TR56 mus musculus
34	841.5	51.9	321	1	052P1_HUMAN	08nh57 homo sapien
35	838.5	51.7	312	2	08VGX6_MOUSE	08VGX6 mus musculus
36	835.5	51.5	314	2	08VH15_MOUSE	08VH15 mus musculus
37	835	51.5	330	2	08VP07_MOUSE	08VP07 mus musculus
38	834	51.4	316	2	08VGX8_MOUSE	08VGX8 mus musculus
39	833.5	51.4	317	2	08VGX8_MOUSE	08VGX8 mus musculus
40	831.5	51.3	316	2	07TR55_MOUSE	07TR55 mus musculus
41	831.5	51.3	317	2	08VG09_MOUSE	08VG09 mus musculus
42	831.5	51.3	319	2	08VGX6_MOUSE	08VGX6 mus musculus
43	831.5	51.3	327	2	08VH28_MOUSE	08VH28 mus musculus
44	831	51.2	312	2	08VH12_MOUSE	08VH12 mus musculus
45	829	51.1	311	2	07TR53_MOUSE	07TR53 mus musculus
46	829	51.1	318	2	08VH16_MOUSE	08VH16 mus musculus
47	827.5	51.0	314	2	08VG85_MOUSE	08VG85 mus musculus
48	827.5	51.0	315	1	05111_HUMAN	08ng15 homo sapien
49	827.5	51.0	315	1	061F85_HUMAN	061F85 homo sapien
50	826	50.9	316	2	08VG79_MOUSE	08VG79 mus musculus
51	825.5	50.9	315	2	08VG75_MOUSE	08VG75 mus musculus
52	824	50.8	317	2	08NGK5_HUMAN	08ngk5 homo sapien
53	823.5	50.8	321	1	051G1_HUMAN	051G1_HUMAN
54	823.5	50.8	321	2	07TRP8_MOUSE	07TRP8 mus musculus
55	823.5	50.8	329	2	08VGX9_MOUSE	08VGX9 mus musculus
56	822.5	50.7	316	2	08VG20_MOUSE	08VG20 mus musculus
57	818.5	50.5	312	2	08VP02_MOUSE	08VP02 mus musculus
58	817	50.4	313	1	051A4_HUMAN	08ng16 homo sapien
59	816.5	50.3	316	2	07TRN7_MOUSE	07TRN7 mus musculus
60	816	50.3	319	2	09YH55_CHICK	09YH55 gallus galli
61	815	50.2	321	2	061FH6_HUMAN	061FH6 homo sapien
62	814.5	50.2	313	2	08VG4_MOUSE	08VG4 mus musculus
63	814	50.2	315	2	08VG23_MOUSE	08VG23 mus musculus
64	812.5	50.1	314	1	052K2_HUMAN	08ngk3 homo sapien
65	812.5	50.1	314	2	061FK4_HUMAN	061FK4 homo sapien
66	811.5	50.0	314	2	08VH21_MOUSE	08VH21 mus musculus
67	811	50.0	321	1	052N4_HUMAN	08ng12 homo sapien
68	811	50.0	321	2	061F77_HUMAN	061F77 homo sapien
69	809.5	49.9	315	2	07TRQ2_MOUSE	07TRQ2 mus musculus
70	809.5	49.9	321	2	08VH20_MOUSE	08VH20 mus musculus
71	808.5	49.8	314	1	052K1_HUMAN	08ngk4 homo sapien
72	808.5	49.8	314	2	061FK5_HUMAN	061FK5 homo sapien
73	808.5	49.8	317	2	06W053_MOUSE	06W053 mus musculus
74	807.5	49.8	315	2	07TRQ3_MOUSE	07TRQ3 mus musculus
75	806.5	49.7	314	1	05111_HUMAN	08ngk3 homo sapien
76	806.5	49.7	314	2	061F93_HUMAN	061F93 homo sapien
77	806	49.7	312	2	08VGW2_MOUSE	08VGW2 mus musculus
78	805.5	49.7	314	2	07TRR0_MOUSE	07TRR0 mus musculus
79	805.5	49.7	321	2	08VH19_MOUSE	08VH19 mus musculus
80	803.5	49.5	314	2	07TRR7_MOUSE	07TRR7 mus musculus
81	803	49.5	326	2	09WV09_MOUSE	09WV09 mus musculus
82	802	49.4	323	2	08VG75_MOUSE	08VG75 mus musculus
83	801.5	49.4	312	1	051A7_HUMAN	08nh64 homo sapien
84	801.5	49.4	312	2	061F88_HUMAN	061F88 homo sapien
85	799.5	49.3	330	1	051F1_HUMAN	08nh61 homo sapien
86	799.5	49.3	342	2	061F11_HUMAN	061F11 homo sapien
87	799	49.3	302	1	051H1_HUMAN	08nh63 homo sapien
88	799	49.3	302	2	061F13_HUMAN	061F13 homo sapien
89	799	49.3	312	1	052E4_HUMAN	08ng18 homo sapien
90	799	49.3	312	2	061F60_HUMAN	061F60 homo sapien
91	799	49.3	313	2	07TRR8_MOUSE	07TRR8 mus musculus
92	799	49.3	317	2	08VH13_MOUSE	08VH13 mus musculus
93	797.5	49.2	322	2	08VGW5_MOUSE	08VGW5 mus musculus
94	796	49.1	316	2	09B005_MOUSE	09B005 mus musculus
95	795	49.0	311	2	07TRK4_MOUSE	07TRK4 mus musculus
96	794	49.0	318	2	08VH14_MOUSE	08VH14 mus musculus
97	794	49.0	318	2	08VG73_MOUSE	08VG73 mus musculus
98	794	49.0	328	2	06W055_MOUSE	06W055 mus musculus
99	793.5	48.9	314	2	08VGY1_MOUSE	08VGY1 mus musculus
100	793.5	48.9	316	2	08VH03_MOUSE	08VH03 mus musculus

ALIGNMENTS

```

RESULT 1
Q6IFP93_HUMAN PRELIMINARY; PRT; 318 AA.
ID Q6IFP93_HUMAN PRELIMINARY; PRT; 318 AA.
AC Q6IFP93;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Olfactory receptor OR11-15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCB1_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14983052; DOI=10.1073/pnas.0307882100;
RA Mainic B., Godfrey P.A., Buck L.B.;
RT "The human olfactory receptor gene family."
RL Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).
CC -1- MSCELANOUS: The sequence shown here is derived from an
EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK004369; DAA04767.1; -; Genomic_DNA.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007166; P:G-protein coupled receptor protein signaln. . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHDOPS.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
KW Receptor.
SQ SEQUENCE 318 AA; 35402 MW; 9412125346584865 CRC64;

Query Match 99.8%; Score 1619; DB 2; Length 318;
Best Local Similarity 99.7%; Pred. No. 1,1e-113;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGESSATYFYLIGLPGLEBAQFWLAFPLCSLYLVNGLTIYVTRSHLSE 60
DB 1 MMVDPNGESSATYFYLIGLPGLEBAQFWLAFPLCSLYLVNGLTIYVTRSHLSE 60
QY 61 PMYIFLCWLSGIDILISTSSMPKMLAIFWPNSTTIQPDACLIQFAHSLSGMESTVLLA 120
DB 61 PMYIFLCWLSGIDILISTSSMPKMLAIFWPNSTTIQPDACLIQFAHSLSGMESTVLLA 120
QY 121 MAPRYYVAICHPLRHATVLTLPYTKIGVAVVRAAAMAPLPVPIKQLPCRSHIISHS 180
DB 121 MAPRYYVAICHPLRHATVLTLPYTKIGVAVVRAAAMAPLPVPIKQLPCRSHIISHS 180
QY 121 MAPRYYVAICHPLRHATVLTLPYTKIGVAVVRAAAMAPLPVPIKQLPCRSHIISHS 180
DB 121 MAPRYYVAICHPLRHATVLTLPYTKIGVAVVRAAAMAPLPVPIKQLPCRSHIISHS 180
QY 181 YCLHQDVWKLACDDIRVNVVYGLYIISALIGDSLISFSYLLIKTYLGLTREAAQAF 240
DB 181 YCLHQDVWKLACDDIRVNVVYGLYIISALIGDSLISFSYLLIKTYLGLTREAAQAF 240
QY 181 YCLHQDVWKLACDDIRVNVVYGLYIISALIGDSLISFSYLLIKTYLGLTREAAQAF 240
DB 181 YCLHQDVWKLACDDIRVNVVYGLYIISALIGDSLISFSYLLIKTYLGLTREAAQAF 240
QY 241 GTCVSHVCAVPIFYVPFGLSMVHRFSRRDSPFLVILANITYLVPLVPIVGVKTXE 300
DB 241 GTCVSHVCAVPIFYVPFGLSMVHRFSRRDSPFLVILANITYLVPLVPIVGVKTXE 300
QY 241 GTCVSHVCAVPIFYVPFGLSMVHRFSRRDSPFLVILANITYLVPLVPIVGVKTXE 300
DB 241 GTCVSHVCAVPIFYVPFGLSMVHRFSRRDSPFLVILANITYLVPLVPIVGVKTXE 300
QY 301 IRRRIILRLFHVATASEP 318
DB 301 IRRRIILRLFHVATASEP 318
QY 301 IRRRIILRLFHVATASEP 318
DB 301 IRRRIILRLFHVATASEP 318

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DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Olfactory receptor 51E1.
GN Name=OR51E1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCB1_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Suwa M., Sato T., Oouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA DiChienko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitley R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -1- DATABASE: NMBE=Human Olfactory Receptor Data Explorerforum
(HORDE);
WWW="http://bip.wetzmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&value=OR51E1";
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; AB065787; BAC06006.1; -; Genomic_DNA.
CC EMBL; BC022401; AA022401.1; -; mRNA.
CC Ensembl; ENSG00000180785; Homo sapiens.
CC HGNC; HGNC:15194; OR51E1.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC InterPro; IPR000725; Olfact_receptor.
CC PANTHER; PTHR11398; Olfact_receptor; 1.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHDOPS.
CC PROSITE; PR00237; G_PROTEIN_REC_P1_1.
CC PROSITE; PS00237; G_PROTEIN_REC_P1_2; 1.
CC PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW Receptor; Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM 1 27
FT TRANSMEM 28 48
FT TOPO_DOM 49 56
FT TRANSMEM 57 77
FT TOPO_DOM 78 101
FT TRANSMEM 102 122

```

Query	Match	Best local similarity	Score	DB	Length
Matches	316	Conservative	1	Mismatches	0
Indels	0	Gaps	0		
Query	2	MDVNGNGSSATYFLILGLPGLEERQFLAPPLCSLYLIVAGNLTITTYVRTSHLSP	61		
Db	1	MDVNGNGSSATYFLILGLPGLEERQFLAPPLCSLYLIVAGNLTITTYVRTSHLSP	60		
Query	62	MYFLCMLSGDILISTSSMPKMAIFPNSTTIOFDACLQIPAIHSLSGMSVLLAM	121		
Db	61	MYFLCMLSGDILISTSSMPKMAIFPNSTTIOFDACLQIPAIHSLSGMSVLLAM	120		
Query	122	AFDRYVAICHELRAHATVTLPRVTKIGVAAYVVGALMAAPLPVKOLPFCRSHLSHSY	181		
Db	121	AFDRYVAICHELRAHATVTLPRVTKIGVAAYVVGALMAAPLPVKOLPFCRSHLSHSY	180		
Query	182	CLHDDVWKLACDDIRVNVVYGLIVTISAIGDLSLISSTYLLIKTVGLTREDAKAPG	241		
Db	181	CLHDDVWKLACDDIRVNVVYGLIVTISAIGDLSLISSTYLLIKTVGLTREDAKAPG	240		
Query	242	TCVSHVCAVPIFYVPPFGLSNVHRPSKRDSPLPYLTINLYLVPVLPNPIYGVKTKEI	301		
Db	241	TCVSHVCAVPIFYVPPFGLSNVHRPSKRDSPLPYLTINLYLVPVLPNPIYGVKTKEI	300		
Query	302	RQRILRLPHVATVTHASEP	318		
Db	301	RQRILRLPHVATVTHASEP	317		
RESULT 3					
Q584P5	HUMAN				
ID	Q584P5	HUMAN	PRELIMINARY	PRT	317 AA.
AC	Q584P5				
DT	01-FEB-2005	(TREMBLrel. 29, Created)			
DT	01-FEB-2005	(TREMBLrel. 29, Last sequence update)			
DT	01-FEB-2005	(TREMBLrel. 29, Last annotation update)			
DE	Prostate overexpressed G protein-coupled receptor.				
GN	Name:POGR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Weng J., Wang J., Cai Y., Itmann M., Liu M.;				
RT	"POGR, a prostate overexpressed G protein-coupled receptor is a				
RL	sentative biomarker for human prostate cancers."				
RT	Submitted (OCT-2004) to the EMBL/Genbank/DBJ databases.				
DR	EMBL: AY75731.1; AAV54110.1; -; mRNA.				
DR	GO: GO:0016021; C: integral to membrane; IEA.				
DR	GO: GO:0004984; F: olfactory receptor activity; IEA.				
DR	GO: GO:0004872; F: receptor activity; IEA.				
DR	GO: GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.				
DR	InterPro: IPR000276; GPCR Rhodosp.				
DR	InterPro: IPR000725; Olfact_receptor.				
DR	Pfam: PF00001; Tm1.1.				
DR	PRINTS: PR00237; GPCRKHODOPSN.				
DR	PRINTS: PR00245; OLFACTORYR.				

DR	PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR	PROSITE; PSS0262; G_PROTEIN_RECP_F1_2; 1.
KW	Receptor.
SQ	SEQUENCE 317 AA; 35271 MW; 8C7293AA7FBCA95C CRC64;
Query Match	99.5%; Score 1614; DB 2; Length 317;
Best Local Similarity	99.7%; Pred. No. 2, 6e-113;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps	
DY	2 MVDPNGNSASATYFILIGLGLBEAQFWLAAPLCISLYIAVLGNLTIIIVRTESLSHP 61
Db	1 MVDPNGNSASATYFILIGLGLBEAQFWLAAPLCISLYIAVLGNLTIIIVRTESLSHP 60
DY	62 MYIFLCMLSGIDILLISTSSMPKRLAFWRNSTTIQDACLQTFALHSLSGMESTVLLM 120
Db	61 MYIFLCMLSGIDILLISTSSMPKRLAFWFNSTTIOFDACILQMFALHSLSGMESTVLLM 122
DY	122 AFRYYVAICPLRHAAVTLTLPRTXKI GVAAVVAGALLMAPLPFIQQLPFCRSNIISHSY 18
Db	121 AFDPYYVAICPLRHAAVTLTLPRTYTKI GVAAVVAGALLMAPLPFIQQLPFCRSNIISHSY 18
DY	182 CLHQDVWKACDDIRVVNVVGYLVIIISAIGLDSLISFSYLLIKLTVLGITREAOAKRG 24
Db	181 CLHQDVWKACDDIRVVNVVGYLVIIISAIGLDSLISFSYLLIKLTVLGITREAOAKRG 2
DY	242 TCVSHVCAVFIPVPPIGTLSMWRFSKRDSPLPVLIANTYLAVPPVNPITYGVTKET 30
Db	241 TCVSHVCAVFIPVPPIGTLSMWRFSKRDSPLPVLIANTYLAVPPVNPITYGVTKET 30
DY	302 RQRILRLEFHVATHASEP 318
Db	301 RQRILRLEFHVATHASEP 317
RESULT 4	
O66X57 HUMAN	
ID	O66X57_HUMAN PRELIMINARY; PRT; 318 AA.
AC	O66X57;
DT	25-OCT-2004 (TrEMBLrel. 28, Created)
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	Dresden-G-protein-coupled receptor.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Prostate;
RX	PubMed=15313197; DOI=10.1016/j.jbcrc.2004.07.106;
RA	Weisling B., Fuesell S., Ebner R., Temme A., Schmitz M., Schwind S.,
RA	Kieseling A., Kieger M.A., Meye A., Bachmann M., Wirth M.P.,
RA	Rieber E.P.;
RT	"D-GPCR: a novel putative G protein-coupled receptor overexpressed in
RT	prostate cancer and prostate."
RL	Biochem. Biophys. Res. Commun. 322:239-249(2004) .
RL	EMBL; AY698056; AAU07996.1; -; mRNA.
DR	Ensembl; ENSG00000180785; Homo sapiens.
DR	GJ; GO:0016021; C:integral to membrane; IEA.
DR	GJ; GO:0004984; F:olfactory receptor activity; IEA.
DR	GJ; GO:0004872; F:receptor activity; IEA.
DR	GO:0007186; P:g-protein coupled receptor protein signaln. . ; IEA.
DR	GO:0007165; P:signal transduction; IEA.
DR	InterPro; IPR000276; GPCR_Rhodopn.
DR	InterPro; IPR000725; Olfact_receptor.
DR	PANTHER; PTHR11398; Olfact_receptor; 1.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHHODOPS.
DR	PRINTS; PR00245; OLFACTORYR.
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR	PROSITE; PSS0262; G_PROTEIN_RECP_F1_2; 1.
KW	Receptor.

SO SEQUENCE 318 AA; 35386 MW; 941212535D324B65 CRC64;

Query Match 99.4%; Score 1612; DB 2; Length 318;
 Best Local Similarity 99.4%; Pred. No. 3.7e-113;
 Matches 316; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIANGLNLTIIYVIRTHSHLHE 60
 DB 1 MMVDPNGNESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIANGLNLTIIYVIRTHSHLHE 60
 QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWNSSTIIQPDACILQIPAHISLSGMSSTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWNSSTIIQPDACILQIPAHISLSGMSSTVLLA 120
 QY 121 MAPRRYVAICHPRLHATVLTLPVTKIGVAAVVGAALMAPLPVPIKOLPCRSNIISHS 180
 DB 121 MAPRRYVAICHPRLHATVLTLPVTKIGVAAVVGAALMAPLPVPIKOLPCRSNIISHS 180
 QY 181 YCLHODVWKLACDDIRVNVVGLIYIISAGLDSILISFSYLLIKTVLGLTREAOAKAF 240
 DB 181 YCLHODVWKLACDDIRVNVVGLIYIISAGLDSILISFSYLLIKTVLGLTREAOAKAF 240
 QY 241 GTCVSHVCAVFIYPVPFIGLSMVHRFSKRDSPLVLIANIYLLVPPVLANPIVGVKTKXE 300
 DB 241 GTCVSHVCAVFIYPVPFIGLSMVHRFSKRDSPLVLIANIYLLVPPVLANPIVGVKTKXE 300
 QY 301 IRORIILRFHVATHASEP 318
 DB 301 IRORIILRFHVATHASEP 318

RESULT 5

Q8VGZ7_MOUSE PRELIMINARY; PRT; 317 AA.

AC Q8VGZ7; 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
 DE Olfactory receptor MOR18-1 (Olfactory receptor Olfr558) (Prostate overexpressed G protein coupled receptor).
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21676863; PubMed=11802173;
 RA Zhang X., Firestein S.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 5:124-133(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
 RA Young J.M., Friedman C., Williams E.M., Rose J.A., Tomnes-Priddy L., Trask B.J.;
 RT "Different evolutionary processes shaped the mouse and human olfactory receptor gene families."
 RL Hum. Mol. Genet. 11:535-546(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
 RA Young J.M., Shykand B.M., Lane R.P., Tomnes-Priddy L., Rose J.A., Walker M., Williams E.M., Trask B.J.;
 RT "Olfactory receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal genome Biol. 4:R71-R71(2003).
 RL Genome Biol. 4:R71-R71(2003).

EN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA Wang J., Wang J., Itmann M., Liu M.;
 RT "PCR, an olfactory G-protein coupled receptor, is overexpressed in human prostate and prostate cancers."
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072993; AA60656.1; -; Genomic DNA.
 DR EMBL; AY317671; AAP71050.1; -; Genomic DNA.
 DR EMBL; AY834217; AA97880.1; -; mRNA.
 DR EMBL; ENSMUSG0000049016; Mus musculus.
 DR MGI; MGI:303092; Olfr558.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004964; F:olfactory receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodan.
 DR InterPro; IPR000725; Olfact_receptor.
 DR PANTHER; PTHR11398; Olfact_receptor; 1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHDOPSN.
 DR PRINTS; PR00245; OLFACTORYR.
 DR PROSITE; PS00237; G_PROTEIN_RECER_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECER_F1_2; 1.
 KW Receptor.
 SO SEQUENCE 317 AA; 35464 MW; 5A0B59E229852534 CRC64;

Query Match 93.2%; Score 1512; DB 2; Length 317;
 Best Local Similarity 93.4%; Pred. No. 1.2e-105;
 Matches 295; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 MWDNGNESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIANGLNLTIIYVIRTHSHLHE 61
 DB 1 MWDNGNESSATYFIIIGLPGLEBAQFWLAFPLCSLYLIANGLNLTIIYVIRTHSHLHE 60
 QY 62 MYIFLCMLSGIDILISTSSMPKMLAIFWNSSTIIQPDACILQIPAHISLSGMSSTVLLAM 121
 DB 62 MYIFLCMLSGIDILISTSSMPKMLAIFWNSSTIIQPDACILQIPAHISLSGMSSTVLLAM 120
 QY 122 AFDRYVAICHPRLHATVLTLPVTKIGVAAVVGAALMAPLPVPIKOLPCRSNIISHSY 181
 DB 122 AFDRYVAICHPRLHATVLTLPVTKIGVAAVVGAALMAPLPVPIKOLPCRSNIISHSY 180
 QY 181 CLHODVWKLACDDIRVNVVGLIYIISAGLDSILISFSYLLIKTVLGLTREAOAKAF 240
 DB 181 CLHODVWKLACDDIRVNVVGLIYIISAGLDSILISFSYLLIKTVLGLTREAOAKAF 240
 QY 242 TCVSHVCAVFIYPVPFIGLSMVHRFSKRDSPLVLIANIYLLVPPVLANPIVGVKTKEI 301
 DB 242 TCVSHVCAVFIYPVPFIGLSMVHRFSKRDSPLVLIANIYLLVPPVLANPIVGVKTKEI 300
 QY 302 RORILRLFHVATHASE 317
 DB 302 RORILRLFHVATHASE 316
 RESULT 6
 OSMD65 RAT PRELIMINARY; PRT; 317 AA.
 ID OSMD65 RAT
 AC OSMD65; 01-FEB-2005 (Tremblrel. 29, Created)
 DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
 DE Prostate overexpressed G protein coupled receptor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Murinae; Rattus.
 NC NCBI_TaxID=10116;

[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=BN;
RA Wang J., Wang J., Ittmann M., Liu M.;
RT "POGR, an olfactory G-protein coupled receptor, is overexpressed in human prostate and prostate cancers.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY834218; AAV97881.1; -; mRNA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004872; F: protein activity; IEA.
DR GO: GO:0004872; F: protein activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signaling. . .; IEA.
DR GO: GO:0007186; P: signal transduction; IEA.
DR InterPro: IPR000276; GPCR_Rhodopn.
DR PANTHER: PTHR11398; Olfact_receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOPOSN.
DR PROSITE: PS00245; OLFACTORYR.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR RECEPTOR.
KM SEQUENCE 317 AA; 35479 MW; C761FD6439D27A26 CRC64;
Query Match 92.4%; Score 1498; DB 2; Length 317;
Best Local Similarity 92.4%; Pred. No. 1.4e-104;
Matches 291; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
QY 2 MVDNGESSATYPTILGLPELEAOFMLAPLCSLYLNAVGLNLTIIYVTEHSLHEP 61
DB 1 MGSBSGESSYTFILGLPELEFQFWLAPLCSLYLNAVGLNLTIIYVTEHSLHEP 60
QY 62 MYFLCMLSGDILISTSMPEKMLAFMNSTTIOFDACILQIPAIHSLSGMESTVLLAM 121
DB 61 MYFLCMLSGDILISTSMPEKMLAFMNSTTIOFDACILQIPAIHSLSGMESTVLLAM 120
QY 122 AFDPRVAICHPRLRATVTLPRVTKIGVAAVVRGAALMAPLPVTKQLPFCRSNIIISHSY 181
DB 121 AFDPRVAICHPRLRATVTLPRVTKIGVAAVVRGAALMAPLPVTKQLPFCRSNIIISHSY 180
QY 182 CLHODVKKACDDIRNVVYGLIYIISALGDSLLISFSYLLIKTVGLTREBAQAKAFG 241
DB 181 CLHODVKKACDDIRNVVYGLIYIISALGDSLLISFSYLLIKTVGLTREBAQAKAFG 240
QY 242 TCVSHVCAVPIFYVPFGLSMVHRFSKRSDSPLVILANITYLVLPVLANPIVGVKTKEI 301
DB 241 TCVSHVCAVPIFYVPFGLSMVHRFSKRSDSPLVILANITYLVLPVLANPIVGVKTKEI 300
QY 302 RORILRLFHVAITMAS 316
DB 301 RORILRLFLMTHTS 315

RESULT 7
Q6SNE2_9PRIM
ID Q6SNE2_9PRIM PRELIMINARY; PRT; 223 AA.
AC Q6SNE2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DS Olfactory receptor (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Gorilla.
OC NCBI_TaxID=9593;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Giald Y., Wiebe V., Przeworski M., Lancel D., Paabo S.;
RT "Loss of Olfactory Receptor Genes Coincides with the Acquisition of Full Trichromatic Vision in Primates.";
RL PLOS Biol. 2:0120-0125(2004).
EMBL: AY454949; AARI9522.1; -; Genom1c_DNA.

DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004872; F: olfactory receptor activity; IEA.
DR GO: GO:0004872; F: protein activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signaling. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopn.
DR InterPro: IPR000725; Olfact_receptor.
DR PANTHER: PTHR11398; Olfact_receptor; 1.
DR PRINTS: PR00245; OLFACTORYR.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR RECEPTOR.
KM NON TER 1 1
FT NON TER 223 223
SQ SEQUENCE 223 AA; 24538 MW; E963757D41480412 CRC64;
Query Match 68.6%; Score 1113; DB 2; Length 223;
Best Local Similarity 98.7%; Pred. No. 8.6e-76;
Matches 220; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 67 CMLSGDILISTSMPEKMLAFMNSTTIOFDACILQIPAIHSLSGMESTVLLAMADRY 126
DB 1 CMLSGDILISTSMPEKMLAFMNSTTIOFDACILQIPAIHSLSGMESTVLLAMADRY 60
QY 127 VAICHPRLRATVTLPRVTKIGVAAVVRGAALMAPLPVTKQLPFCRSNIIISHSYCLHOD 186
DB 61 VAICHPRLRATVTLPRVTKIGVAAVVRGAALMAPLPVTKQLPFCRSNIIISHSYCLHOD 120
QY 187 VMKLCADDIRNVVYGLIYIISALGDSLLISFSYLLIKTVGLTREBAQAKAFGTCVSH 246
DB 121 VMKLCADDIRNVVYGLIYIISALGDSLLISFSYLLIKTVGLTREBAQAKAFGTCVSH 180
QY 247 VCAVPIFYVPFGLSMVHRFSKRSDSPLVILANITYLVLPV 289
DB 181 VCAVPIFYVPFGLSMVHRFSKRSDSPLVILANITYLVLPV 223

RESULT 8
Q8VBV9_MOUSE
ID Q8VBV9_MOUSE PRELIMINARY; PRT; 320 AA.
AC Q8VBV9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DS Olfactory receptor MOR18-2 (Olfactory receptor Olfr78) (Prostate-specific G protein-coupled receptor RalG) (Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631413D08 DE product: Olfactory Receptor MOR18-2, full insert sequence) (Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630060D12 product: Olfactory Receptor MOR18-2, full insert sequence).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINB=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 5:124-133(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINB=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L., Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory receptor gene families.";
RL Hum. Mol. Genet. 11:535-546(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

[4]
RA NUCLEOTIDE SEQUENCE.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykina B.M., Lane R.P., Tomes-Priddy L., Rose J.A.,
RA Walker M., Williams E.M., Traak B.J.;
RT "Olfactory receptor expressed sequence tags demonstrate olfactory
RT expression of over 400 genes, extensive alternate splicing and unequal
RT expression levels";
RL Genome Biol. 4:R71-R71(2003).
RN
RN NUCLEOTIDE SEQUENCE.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=BA1B/C;
RX MEDLINE=21564169; PubMed=11707321; DOI=10.1016/S0378-1119(01)00709-0;
RA Yuan T.T., Toy P., McClary J.A., Lin R.D., Miyamoto N.G.,
RA Kretschmer P.J.;
RT "Cloning and genetic characterization of an evolutionarily conserved
RT human olfactory receptor that is differentially expressed across
RT species";
RL Gene 278:41-51(2001).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Meth. Enzymol. 303:19-44(1999).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuhl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Stubbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga M., Carninci P., de Bonaldo M.F.,
RA Bormstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wiltaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 403:665-690(2001).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nishikido I., Oshio N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yagi K., Tomaru A., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schiraldi L.M., Knapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dregani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Karai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurckin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Matsuda L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwa K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsuzawa S., Kawai J.,
RA Kiyosawa Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuhl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Stubbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga M., Carninci P., de Bonaldo M.F.,
RA Bormstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wiltaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 403:665-690(2001).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nishikido I., Oshio N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yagi K., Tomaru A., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schiraldi L.M., Knapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dregani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Karai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurckin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Matsuda L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Query Match 60.7%; Score 985; DB 2; Length 320;
Best local similarity 59.8%; Pred. No. 5e-66;

Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;

QY 8 NBSATYVILGLPGLBEAQFWLAPLCSLYLAVLGNLTIIYRTSHSLHEPMYFLC 67
 DB 5 NPTHTAT-FVLIGIPLEKQHFVWGFPPLSMVYVAMFGNCIVFVIRTERSLHAPMYFLC 63
 QY 68 MLSGIDILISTSSMPKMLAIFMFSNTTIOFDACLIQIFAIHSLSGMESVTLIAMAEDRYV 127
 DB 64 MLAIDILISTSSMPKMLAIFMFSNTTIOFDACLIQIFAIHSLSGMESVTLIAMAEDRYV 123
 QY 128 AICHPLRHATVLTLPRTVKIGVAAVRGAAALMAPLPVFIKQLPFCRSNITLSHSCYCLHODV 187
 DB 124 AICHPLRHAAVLTNTVTAQIGIVAAVKGSLPFPPLPLIKRLAFCHSNVLSHSCYCLHODV 183
 QY 188 MKLACDDIRNVVYVGLVLIISALIGDSLISPSYLLIKTVLGL-TREBAQKAGTCVSH 246
 DB 184 MKLAVADTLPRVYVGLTALILVMGVDMFISLYFLIRTVLQPLSKERAKAPCTCVSH 243
 QY 247 VCAVFIYPVPIGSLMVRFSKRSDPLPVLIANIYLLVPPVLPNIYGVTKKEIRORIL 306
 DB 244 IGVTLAFVPLIGLSVHRFQNSLHPVIRVVMGDIYLLPPVINPIYIGAKTKQIRTRVL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

RESULT 10

Q6IF94_HUMAN

ID Q6IF94_HUMAN PRELIMINARY; PRT; 320 AA.

AC Q6IF94; 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Olfactory receptor OR11-16.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

NCBI_Taxid=9606;

[1]

RX NUCLEOTIDE SEQUENCE.

RP PubMed:14983052; DOI=10.1073/pnas.0307882100;

RA Malnic B.; Godfrey P.A.; Buck L.B.;

RT "The human olfactory receptor gene family."

RL Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).

DR EMBL; BK004368; DA04766.1; -; Genomic DNA.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0004964; F:Olfactory receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR InterPro; IPR000725; Olfact_receptor.

DR Pfam; PF00001; 7tm.1.1.

DR PRINTS; PR00237; GPCR_RHODPSN.

DR PRINTS; PR00245; OLFACTORYR.

DR PROSITE; PS00237; G_PROTEIN_RECBP_F1_1; UNKNOWN_1.

DR PROSITE; PS0262; G_PROTEIN_RECBP_F1_2; 1.

KM Receptor.

SQ SEQUENCE 320 AA; 35493 MW; 03582CC2AAB6R2C6 CRC64;

Query Match 60.4%; Score 979; DB 2; Length 320;
 Best Local Similarity 59.5%; Pred. No. 1.4e-65;
 Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;

QY 8 NBSATYVILGLPGLBEAQFWLAPLCSLYLAVLGNLTIIYRTSHSLHEPMYFLC 67
 DB 5 NPTHTAT-FVLIGIPLEKQHFVWGFPPLSMVYVAMFGNCIVFVIRTERSLHAPMYFLC 63
 QY 68 MLSGIDILISTSSMPKMLAIFMFSNTTIOFDACLIQIFAIHSLSGMESVTLIAMAEDRYV 127
 DB 64 MLAIDILISTSSMPKMLAIFMFSNTTIOFDACLIQIFAIHSLSGMESVTLIAMAEDRYV 123

QY 128 AICHPLRHATVLTLPRTVKIGVAAVRGAAALMAPLPVFIKQLPFCRSNITLSHSCYCLHODV 187
 DB 124 AICHPLRHAAVLTNTVTAQIGIVAAVKGSLPFPPLPLIKRLAFCHSNVLSHSCYCLHODV 183
 QY 188 MKLACDDIRNVVYVGLVLIISALIGDSLISPSYLLIKTVLGL-TREBAQKAGTCVSH 246
 DB 184 MKLAVADTLPRVYVGLTALILVMGVDMFISLYFLIRTVLQPLSKERAKAPCTCVSH 243
 QY 247 VCAVFIYPVPIGSLMVRFSKRSDPLPVLIANIYLLVPPVLPNIYGVTKKEIRORIL 306
 DB 244 IGVTLAFVPLIGLSVHRFQNSLHPVIRVVMGDIYLLPPVINPIYIGAKTKQIRTRVL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

RESULT 11

O51E2_RAT

ID O51E2_RAT STANDARD; PRT; 320 AA.

AC O51E2; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Olfactory receptor O51E2 (G-protein coupled receptor RALC).

GN Name=O51e2;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Rattus.

NCBI_Taxid=10116;

[1]

RX NUCLEOTIDE SEQUENCE.

RP TISSUE=Brain;

RA MEDLINE:99131082; PubMed:9932290;

RT "Identification of a novel G-protein coupled receptor expressed in

RL distinct brain regions and a defined olfactory zone."

RT Recept. Channels 6:141-151(1998).

CC -1- FUNCTION: Putative odorant receptor.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Expressed only in some areas of the brain and

CC in the olfactory epithelium.

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

DR EMBL; AF079864; AA012761.1; -; mRNA.

DR EMBL; ENSRN00000018606; Rattus norvegicus.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR InterPro; IPR000725; Olfact_receptor.

DR PANTHER; PTHR11398; Olfact_receptor; 1.

DR Pfam; PF00001; 7tm.1.1.

DR PRINTS; PR00237; GPCR_RHODPSN.

DR PRINTS; PR00245; OLFACTORYR.

DR PROSITE; PS00237; G_PROTEIN_RECBP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECBP_F1_2; 1.

KM G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;

KM Receptor; Sensory transduction; Transducer; Transmembrane.

FT TOPO_DOM 1 24 1 (Potential)

FT TRANSMEM 25 45 1 (Potential)

FT TOPO_DOM 46 53 2 (Potential)

FT TRANSMEM 54 74 2 (Potential)

FT TOPO_DOM 75 98 3 (Potential)

FT TRANSMEM 99 119 3 (Potential)

FT TOPO_DOM 120 138 4 (Potential)

FT TRANSMEM 139 159 4 (Potential)

FT TOPO_DOM 160 195 5 (Potential)

FT TRANSMEM 196 216 5 (Potential)

FT	TOPO_DOM	217	236	Cytoplasmic (Potential).
FT	TRANSMEM	237	257	6 (Potential).
FT	TOPO_DOM	258	272	Extracellular (Potential).
FT	TRANSMEM	273	293	7 (Potential).
FT	TOPO_DOM	294	320	Cytoplasmic (Potential).
FT	CARBOHYD	5	5	N-linked (GlcNAc...) (potential).
FT	DISULFID	96	178	By similarity.
SO	SEQUENCE	320 AA;	35505 MW;	87PF78F5PFD5BP94 CRC64;
Query Match		60.2%;	Score 977;	DB 1; Length 320;
Best Local Similarity		59.5%;	Pred. No. 2e-65;	
Matches	182;	Conservative	53;	Mismatches 69; Indels 2; Gaps 2
QY	:	:	:	:
8	NESSATYELILGLPGLBEAQFWLAPPLCSLYLAVLGNLTIIYVRTESHLBPMYFLC	67		
5	NFTNAT-PMLIGIPELBEAHFWGFPPLSMVAVLFGNCIVFVIRTERSLHAPYLLFLC	63		
QY	:	:	:	:
68	MLSGDILISYSSMKNKALAPFNSSTIQFDALQIPAIHLSGMSGVLLMAFPDRY	127		
64	MLAAILDLASTYSEPKIALFWPDSRETRTPDACLQMFPIHLSAIESITLLAMAFDRY	123		
QY	:	:	:	:
128	AICHPLRATVLTLPRTVTKIGVAAVRGALMAAPVPVFIKOLPFRSNILSHCYADQV	187		
124	AICHPLRDAALNTVTVQIGVALVRKSLPFPFPLIKRLAFGSHVLSISYCVHDV	183		
QY	:	:	:	:
188	MKLACDDIRVAVVYGLIVIIISAIGDSLISPSYLLIKTVLGL-TREAQAYAFQCVSH	246		
184	MKLAVTDLTPVNVYGLTALILWGVDMWFIISLYELIRAVLQLPSKSRBAVAFQCVSH	243		
QY	:	:	:	:
247	VCANFIFVYVPFPGISLMSWRFSGRRSPPLVILANTLYLVPPPLANTIVGVTKERQRL	306		
244	IGVVLAFVYVPLIGLSVHRFGNSLDPIVHVLMDVYLLLPVINPIIYGAKTKQIRTRVL	303		
QY	:	:	:	:
307	RLPFHYA	312		
QY	:	:	:	:
304	AMFKIS	309		
Db				
RESULT 12				
Q8VF09	MOUSE			
ID	Q8VF09_MOUSE PRELIMINARY;	PRT;	322 AA.	
AC	Q8VF09;			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	01-FEB-2005 (Tremblrel. 29, Last annotation update)			
DE	Olfactory receptor MOR18-3 (Olfactory receptor Olfr557).			
GN	Name=Olfr557;			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
OX	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RP	MDLINE=21676863; PubMed=11802173;			
RA	Zhang X., Firestein S.;			
RA	"The olfactory receptor gene superfamily of the mouse."			
RA	Nat. Neurosci. 5:124-133(2002).			
RL	[2]			
RN	NUCLEOTIDE SEQUENCE.			
RP	MDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;			
RA	Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,			
RA	Trask B.J.;			
RT	"Different evolutionary processes shaped the mouse and human olfactory			
RT	receptor gene families."			
RL	Hum. Mol. Genet. 11:535-546(2002).			
RL	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RP	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
RP	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RP	MDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;			

Query	Match	Score	DB	Length
Query Match	59.6%	Score 967.5;	DB 2;	Length 322;
Best local similarity	58.2%;	Pred. No. 1e-64;		
Matches 181;	Conservative 59;	Mismatches 68;	Indels 3;	Gaps 3;
RA	Young J.M., Shykind B.M., Lane R.P., Tomnes-Priddy L., Ross J.A.,			
RA	Walker M., Williams E.M., Trask B.U.;			
RA	"Odorant receptor expressed sequence tags demonstrate olfactory			
RT	expression of over 400 genes, extensive alternate splicing and unequal			
RT	expression levels".			
RL	Genome Biol. 4:R71-R71 (2003).			
RL	[5]			
RN	NUCLEOTIDE SEQUENCE.			
RP	Sanders K.;			
RA	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AY137670; AAP11049.1; -; Genomic DNA.			
DR	EMBL; AY073732; AAL61395.1; -; Genomic DNA.			
DR	Ensembl; ENSMUSG0000046017; Mus musculus.			
DR	MGI; MGI:3030391; Olfir557.			
GO	GO:0016021; C:integral to membrane; IEA.			
DR	GO:0004984; F:olfactory receptor activity; IEA.			
DR	GO:0004872; F:receptor activity; IEA.			
DR	GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.			
DR	GO:0007185; P:signal transduction; IEA.			
DR	InterPro; IPR000726; GPCR_Rhodopsn.			
DR	InterPro; IPR000725; Olfact_receptor.			
DR	PANTHER; PTHR1398; Olfact_receptor; 1.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PRO0237; GPCR_RHODPSN.			
DR	PRINTS; PRO0245; OLFACTORXR.			
DR	PROSITE; PS00237; G_PROTEIN_RECCEP_F1_1; UNKNOWN_1.			
DR	PROSITE; PS50262; G_PROTEIN_RECCEP_F1_2; 1.			
KW	RECEPTOR.			
SEQ	SEQUENCE 322 AA; 35612 MW; D40302762D4B2FPE CRC64;			
1	MMVDPNNGESATYPIILGLRGL-EEQFWLAPLCSLYLAVLGNLTIIYVTEHSIH 59			
2	::: : : : : : : : : : : : 67			
3	8 LIAPNSLAPALPAFLVLGVIPGLSKIHFWLAPLCPMTAVATGNLALITFIVERRLH 67			
4	60 EPMYIFCMLSGIDILISTSMPTMLAIWFNSTTIOFDACLIQIPAIHSIGNESTVLL 119			
5	: : : : : : : : : : : 127			
6	68 EPMYIFLPMSTIDLVLSSTVPMQABLFLTGIOIEFNICLTQMFILHLSMNEASVLL 127			
7	120 AMAEDRYVAICPLRHATVTLTPRVTIKIYGAVAVVRGAALNAPLDFVFIKQLEFCRSNIIHS 179			
8	128 AMAEDRYVAICPLRHATVTLTPRVTIKIYGAVAVVRGAALNAPLDFVFIKQLEFCRSNIIHS 187			
9	180 SYCHADQWMLACDDIRNVNYYGLIVTISAGLDSLLISYSYLLIKTVLGL-TREDAQK 238			
10	188 SFCLHODIMKLSCHDTKTVNYYGFIILISWGVDSLLIGFSYIILDAVELSTRGALK 247			
11	239 AFGCVSHVCAVFTFYVPFISGLSWHFRSKRDSPLFVILIANIYLVLPVLPNPIYGVKT 298			
12	248 AFWTCISHLCAVLFYVPLIGLSVVAHLG-GPTSLVYHIVNANITLLPVPVNPPIYGAKT 306			
13	299 KEIRORILRLE 309			
14	307 KEIRSVIRME 317			
15	RESULT 13			
16	OSID1_HUMAN STANDARD; PRT; 324 AA.			
17	OSID1_HUMAN STANDARD; PRT; 324 AA.			
18	OSID1_HUMAN STANDARD; PRT; 324 AA.			
19	OSID1_HUMAN STANDARD; PRT; 324 AA.			
20	OSID1_HUMAN STANDARD; PRT; 324 AA.			
21	OSID1_HUMAN STANDARD; PRT; 324 AA.			
22	OSID1_HUMAN STANDARD; PRT; 324 AA.			
23	OSID1_HUMAN STANDARD; PRT; 324 AA.			
24	OSID1_HUMAN STANDARD; PRT; 324 AA.			
25	OSID1_HUMAN STANDARD; PRT; 324 AA.			
26	OSID1_HUMAN STANDARD; PRT; 324 AA.			
27	OSID1_HUMAN STANDARD; PRT; 324 AA.			
28	OSID1_HUMAN STANDARD; PRT; 324 AA.			
29	OSID1_HUMAN STANDARD; PRT; 324 AA.			
30	OSID1_HUMAN STANDARD; PRT; 324 AA.			
31	OSID1_HUMAN STANDARD; PRT; 324 AA.			
32	OSID1_HUMAN STANDARD; PRT; 324 AA.			
33	OSID1_HUMAN STANDARD; PRT; 324 AA.			
34	OSID1_HUMAN STANDARD; PRT; 324 AA.			
35	OSID1_HUMAN STANDARD; PRT; 324 AA.			
36	OSID1_HUMAN STANDARD; PRT; 324 AA.			
37	OSID1_HUMAN STANDARD; PRT; 324 AA.			
38	OSID1_HUMAN STANDARD; PRT; 324 AA.			
39	OSID1_HUMAN STANDARD; PRT; 324 AA.			
40	OSID1_HUMAN STANDARD; PRT; 324 AA.			
41	OSID1_HUMAN STANDARD; PRT; 324 AA.			
42	OSID1_HUMAN STANDARD; PRT; 324 AA.			
43	OSID1_HUMAN STANDARD; PRT; 324 AA.			
44	OSID1_HUMAN STANDARD; PRT; 324 AA.			
45	OSID1_HUMAN STANDARD; PRT; 324 AA.			
46	OSID1_HUMAN STANDARD; PRT; 324 AA.			
47	OSID1_HUMAN STANDARD; PRT; 324 AA.			
48	OSID1_HUMAN STANDARD; PRT; 324 AA.			
49	OSID1_HUMAN STANDARD; PRT; 324 AA.			
50	OSID1_HUMAN STANDARD; PRT; 324 AA.			
51	OSID1_HUMAN STANDARD; PRT; 324 AA.			
52	OSID1_HUMAN STANDARD; PRT; 324 AA			

```

RN NUCLEOTIDE SEQUENCE.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsunoto S.,
RA Tetsunmi S., Aburatani H., Asai K., Akiyama Y.: Analysis of human seven transmembrane helix
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP IDENTIFICATION.
RX PubMed:14983052; DOI=10.1073/pnas.0307882100;
RA Mainic B., Godfrey P.A., Buck L.B.: "The human olfactory receptor gene family."
RT Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -1- DATABASE: NMR-Human Olfactory Receptor Data Explorer
(HORDE)
WWW="http://bip.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&value=ORS1D
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB065855; BAC06073.1; -; Genomic DNA.
CC EMBL; BK004370; DA04768.1; -; Genomic DNA.
CC Ensembl; ENSG00000197428; Homo sapiens.
CC HGNC; HGNC:15193; ORS1D.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC InterPro; IPR000725; Olfact_receptor.
CC PANTHER; PTHR11398; Olfact_receptor; 1.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PRINTS; PR00245; OLFACTOCTR.
CC PROSITE; PS00237; G_PROTEIN_RECPT_P1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECPT_P1_2; 1.
CC G-protein coupled receptor; Multigene family; Olfaction; Receptor;
KM Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM 1 38 Extracellular (Potential).
FT TRANSHEM 39 59 1 (Potential).
FT TOPO_DOM 60 67 Cytoplasmic (Potential).
FT TRANSHEM 68 88 2 (Potential).
FT TOPO_DOM 89 112 Extracellular (Potential).
FT TRANSHEM 113 133 3 (Potential).
FT TOPO_DOM 134 152 Cytoplasmic (Potential).
FT TRANSHEM 153 173 4 (Potential).
FT TOPO_DOM 174 209 Extracellular (Potential).
FT TRANSHEM 210 230 5 (Potential).
FT TOPO_DOM 231 250 Cytoplasmic (Potential).
FT TRANSHEM 251 271 6 (Potential).
FT TOPO_DOM 272 285 Extracellular (Potential).
FT TRANSHEM 286 306 7 (Potential).
FT TOPO_DOM 307 324 Cytoplasmic (Potential).
FT DISULFID 110 202 By similarity.
SQ SEQUENCE 324 AA; 35839 MW; 52401F88565E3BD1 CRC64;
Query March 57.8%; Score 937.5; DB 1; Length 324;
Blast Local Similarity 58.5%; Pred. No. 1.9e-62;
Matches 179; Conservative 52; Mismatches 72; Indels 3; Gaps 3;

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QY 185 QDVAKLACDDIRVVVYGLIYVISAIGLDSLISFSYLLILKTVLGH-TREAQKARGTC 243
DB 195 QDINKSCSTIRVVVYGLIYVISAIGLDSLISFSYLLILKTVLGH-TREAQKARGTC 254
QY 244 VSHVCAVPIFYVPIFGISGMVHRSKRSDPLVILANIYLLVPPVLPPIYGVKTKIRQ 303
DB 255 ISHLCAVLPVFPVPIFGISGMVHRSKRSDPLVILANIYLLVPPVLPVVGATKTKICS 313
QY 304 RIILPLF 309
DB 314 RVLQMF 319
RESULT 14
QYH05 MOUSE
ID QYH05_MOUSE PRELIMINARY; PRT; 315 AA.
AC QYH05;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Olfactory receptor MOR10-1 (Olfactory receptor Olfr555).
GN Name=Olfr555;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 5:124-133(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RA Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory
RT receptor gene families."
RL Hum. Mol. Genet. 11:535-546(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
RT expression of over 400 genes, extensive alternate splicing and unequal
RT expression levels."
RL Genome Biol. 4:R71-R71(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072983; AA060646.1; -; Genomic DNA.
DR EMBL; AY317668; AAP1047.1; -; Genomic DNA.
DR Ensembl; ENSMUSG00000049196; Mus musculus.
DR MGI; MGI:3030389; Olfr555.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.

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DR PRINTS: PR00245; OLFACTORR.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 315 AA; 35157 MW; BAA50EP96683F0A9 CRC64;

Query Match 56.4%; Score 914.5; DB 2; Length 315;
Best Local Similarity 54.5%; Pred. No. 9.7e-61;
Matches 166; Conservative 65; Mismatches 74; Indels 1; Gaps 1;

QY 3 VDPNGESSATYFLLGLPGLEAQMFLAPLCSLYLAIVGNLTIYIVRTSHSLRPM 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MNSNAQTNHSHSLTGLTGMPPDKMPMAPLGLVTLTLNGTILAIVKQSLRPM 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 YIFLCMLSGIDILISTSMRPMALIFWFSNTTIOFDACLIQIPALHSLGSESTVLAMA 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 YFELCTIALDVSLSNSTLPSMLIFWFNAPRIPEFDACIQMFPIHFGVVGSLVMSA 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 FDRYVAICHPLRHATVTLRVTKIGVAAVVGAALMAPLPVPIKOLPGRSNILSHYC 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 FDRFVALRDLPRYASILTHGLIGKGLVAVARACVFPVFPPLIKRLPFCRSNVLSHSC 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 183 LHQDVMLACDDIRVNVVYGLIVISAIGDSLISFSYLLIKTVGL-TREAOAKAFG 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 LHQDAPRLACASTRVNSLYGLIVILTLGDLALILFSYLLIKTVGLISRAERLKAAN 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 TCYSHVCAVPIFYVPFGLSMWHRFSRRDSPLEVIILANILYLLVPVLANPIYGVKTKET 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 TGLSHICAVLIFYPLIGATMIRFGKGLSPVVMFMANILYLLPVLNPIVSVTKTKQI 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 RRRILRLP 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 301 RRRILQVF 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
08VH11_MOUSE PRELIMINARY; PRT; 312 AA.
AC 08VH11;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DB Olfactory receptor MORF-2 (Olfactory receptor Olfr577).
GN Name=Olfr577; (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21676863; Pubmed=11802173;
RX Zhang X., Fierstein S.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 5:124-133(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21864068; Pubmed=11875048; DOI=10.1093/hmg/11.5.535;
RX Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RT Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory
RT receptor gene families.";
RL Hum. Mol. Genet. 11:535-546(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[4]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22974002; Pubmed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RX Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RX Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory

```

```

RT expression of over 400 genes, extensive alternate splicing and unequal
RT expression levels.";
RT Genome Biol. 4:R71-R71(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY072977; AAL60640.1; -; Genomic DNA.
DR EMBL: AY171692; AAF71065.1; -; Genomic DNA.
DR EMBL: ENSMUSG00000043354; Mus musculus.
DR MG1: MG1.3030411; Olfr577.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004984; P:olfactory receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000276; GPCR Rhodopn.
DR InterPro: IPR000725; Olfact_receptor.
DR PANTHER: PTHR11398; Olfact_receptor; 1.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPSN.
DR PRINTS: PR00245; OLFACTORR.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 312 AA; 34575 MW; CD233B373205285 CRC64;

Query Match 55.6%; Score 901.5; DB 2; Length 312;
Best Local Similarity 53.2%; Pred. No. 9.2e-60;
Matches 165; Conservative 63; Mismatches 81; Indels 1; Gaps 1;

QY 1 MMDPNGESSATYFLLGLPGLEAQMFLAPLCSLYLAIVGNLTIYIVRTSHSLR 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MTPGFLNGSMSSSTFLSGIPGLEHMIWISLPLCLMTYLSILGNCITLILIKTESPLR 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 PMTIFLCMLSGIDILISTSMRPMALIFWFSNTTIOFDACLIQIPALHSLGSESTVLAMA 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 PMTIFLCMLALTLGSLCTLPVTLGIFWVGADIDSHDCEPTQFLRHCSPLESSVLTS 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 MAFDRYVAICHPLRHATVTLRVTKIGVAAVVGAALMAPLPVPIKOLPFCRSNVLSHS 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 MAFDRFVALRDLPRYASILTHGLIGKGLVAVARACVFPVFPPLIKRLPFCRSNVLSHSC 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 183 LHQDVMLACDDIRVNVVYGLIVISAIGDSLISFSYLLIKTVGL-TREAOAKA 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 YCHLQEVMLACADIRANSTYGMFIVSVTVGVDLILFSYALILRTVLSIASRAERLKA 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 240 FGTCSHVCAVPIFYVPFGLSMWHRFSRRDSPLEVIILANILYLLVPVLANPIYGVKTK 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 LMTCVSHISAVLLFTYPMIGLSYIHRFGKQAPHLVQVVMGFVLLPFPVNPPIVSVTK 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 EIRORILRLP 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 301 QIRDRVAAHF 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 16
05IG2_HUMAN STANDARD; PRT; 314 AA.
ID 05IG2_HUMAN
AC 08NGKO;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Olfactory receptor 51g2.
GN Name=OR51G2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,

```

Takemura S., Aburatani H., Asai K., Akiyama Y.;
Genome-wide discovery and analysis of human seven transmembrane helix
receptor genes.";
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Putative odorant receptor.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC - DATABASE: NAME=human Olfactory Receptor Data Explorer
(HORD);
WWW="http://db.welmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&val=ORS101"

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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB065794; BAC06013.1; -; Genomic DNA.
DR Ensembl; ENSG00000176893; Homo sapiens.
DR HGNC; HGNC:15198; ORS1C2;
DR InterPro; IPR000276; GPCR_Rhodopn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; Tcm_1; 1.
DR PRINTS; PR00237; GPCRHODOPRN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS02622; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW Receptor; Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM 1 30 Extracellular (Potential).
FT TRANSMEM 31 51 Cytoplasmic (Potential).
FT TOPO_DOM 52 59 Extracellular (Potential).
FT TRANSMEM 60 80 Extracellular (Potential).
FT TOPO_DOM 81 104 Extracellular (Potential).
FT TRANSMEM 105 125 Cytoplasmic (Potential).
FT TOPO_DOM 126 144 Extracellular (Potential).
FT TRANSMEM 145 165 Extracellular (Potential).
FT TOPO_DOM 166 201 Extracellular (Potential).
FT TRANSMEM 202 222 Cytoplasmic (Potential).
FT TOPO_DOM 223 242 Cytoplasmic (Potential).
FT TRANSMEM 243 263 Extracellular (Potential).
FT TOPO_DOM 264 278 Extracellular (Potential).
FT TRANSMEM 279 299 Cytoplasmic (Potential).
FT TOPO_DOM 300 314 N-linked (GLCNAC...) (potential).
FT CAROXYD 8 8 By similarity.
FT DISULFD 102 194
SQ SEQUENCE 314 AA; 35012 MW; 97DD37E1F3B8976C CRC64;

Query Match 55.0%; Score 892.5; DB 1; Length 314;
Best Local Similarity 52.5%; Pred. No. 4, 4e-59;
Matches 160; Conservative 63; Mismatches 81; Indels 1; Gaps 1;

6 NGNESSATYFILIGPLEBEAQFWLAFLPCLSYLIAVAGNTLIIVYHTSHLPMTIF 65
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
8 NSSSSVSATFLSLSGIPGLERMHIWISIPCLFYLVISPGNCTIIFIITKTSLSHPMFLF 67
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
6 LCMLSGIILISTSSMPKMLAIFENNSTTIQPDACLQIFAHSLSGMESTYLMAADRD 125
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
68 LSMALIDIGSLCTLPTVLGIFWVGARIISHDACPAQLFHCHSPLESSVLSMAAFRD 127
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
126 VYAIGHPLRHATVLTLPRTVKIGNAAVVVRGAMAPLPFIQDLFCRSNIISHSYCLHQ 185
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
128 FVALICHLPHLYSIILNTVIYGRIGVSLGRSVALLIFPLPMKLKRPYCSPVLSHYCYLHQ 187
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
186 DVMKLACDDIRVVNVVYGLIVTISAIGLDLLISPSYTLILKTVTGLGTBAQA-KAFGVCV 244
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
188 EVMKLACADMKANSTYGMFVIYSTVGIDSLILFLFYALILRTVLSIASRAERFKLANVCV 247
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
245 SHVCAVFPIPVYFPIGLSNWHRFSPKRDSPLPYILANIVYLVVPNPVIYVGKTEIKOR 304
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
248 SHICAVLLPYTMIGLSVTHRGKQAPHLVQVWGGEMTLFFPPVANPVIYSYKTIQINDR 307
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

QY	305	ILRLP	309
DB	308	VTNAP	312

RESULT 17			
ID	Q61FH7_HUMAN	PRT;	314 AA.
AC	Q61FH7_		
DT	05-JUL-2004 (Tremblrel. 27, Created)		
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)		
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)		
DS	Olfactory receptor OR11-28.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	PubMed=14983052; DOI=10.1073/pnas.0307882100;		
RA	Malnic B., Godfrey P.A., Buck L.B.;		
RT	"The human olfactory receptor gene family".		
RL	Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).		
DR	EMBL; BK004285; DAA04683.1; -; Genomic DNA.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0004984; F:olfactory receptor activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	InterPro; IPR007251; Olfact_receptor.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCR_RHODOPSN.		
DR	PRINTS; PR00245; OLFACTORYR.		
DR	PROSITE; PS00237; G_PROTEIN_RECER_F1_1; UNKNOWN_1.		
DR	PROSITE; PS50262; G_PROTEIN_RECER_F1_2; 1.		
KW	Receptor.		
SQ	SEQUENCE 314 AA; 35012 MW; 97DD37E1F38E976C CRC64;		

Query Match 55.0%; Score 892.5; DB 2; Length 314;			
Best Local Similarity 52.5%; Pred. No. 4.4e-59;			
Matches	160;	Conservative	63; Mismatches 81; Indels 1; Gaps 1;
QY	6	NGNESSATYPLILCPGLEBAQFWLAPLCSGLYLIANVLGNLTYYIVRTESLSHPWTIF	65
DB	8	NSSSSVATFPLISGIPGLERHMIWISPLCFMYLVISIPGCTIIFIKTERSLHPMYLF	67
QY	66	LCMLSGDIIILISTSMPEMLAIFWENSTIOPDACLQIPAIHSLSGMESTVLAMAFDR	125
DB	68	LSMLALIDLGSLCTLPVTVLGIFWVGAREISHDCPQQLPFTHCFSPLESSVLSMAFDR	127
QY	126	VYALICHPRLHATVTLTLPVTKIGVAAVVRCAGALMAPLPVPIKQLPFCRSNLTLSYCLHQ	185
DB	128	FVALICHPRLHATVTLTLPVTKIGVAVVRCAGALMAPLPVPIKQLPFCRSNLTLSYCLHQ	187
QY	186	DWMLGADDLRVNVVVGGLVVISIAGDLSLISSYLLIKTVGLTRBAQA-KAFGCV	244
DB	188	EVMGLGADDMKANSIYGMFVLSVTSVIGDSLILFYSALIKTVGLTRBAQA-KAFGCV	247
QY	245	SHVCAVEIFVYPPFGLSMVRHSRRDPSPLFVILANIYLLVPPVLPNIYVGVTKESIROR	304
DB	248	SHICAVALLFTYPMIGLSVIRHFGQAGHLVGVVWGMFYLLFPVMMPIVVSVKTKQLRDR	307
QY	305	ILRLP	309
DB	308	VTNAP	312

RESULT 18			
ID	Q8VH17_MOUSE	PRT;	313 AA.
AC	Q8VH17_		
DT	01-MAR-2002 (Tremblrel. 20, Created)		

DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, last annotation update)
DE Olfactory receptor MOR7-1 (Olfactory receptor Olfr578).
GN Name=Olfr578;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RL "The olfactory receptor gene superfamily of the mouse."; Nat. Neurosci. 5:124-133(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.;
RL "Different evolutionary processes shaped the mouse and human olfactory receptor gene families."; Hum. Mol. Genet. 11:535-546(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A., Walker M., Williams E.M., Trask B.J.;
RL "Odorant receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels."; Genome Biol. 4:R71-R71(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072971; AL60634.1; -; Genomic DNA.
DR EMBL; AY317693; AAP71066.1; -; Genomic DNA.
DR Ensembl; ENSMUSG00000045792; Mus musculus.
DR MGI; MGI:3030412; Olfr578
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PRINTS; PR00245; OLFACORXR.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
DR KEGG; K04400; GPCR.
SQ SEQUENCE 313 AA; 35682 MW; 39476B03FD201D6C CRC64;
Query Match 54.1%; Score 877; DB 2; Length 313;
Best Local Similarity 51.8%; Pred. No. 6.4e-58;
Matches 156; Conservative 72; Mismatches 73; Indels 2; Gaps 2;

DB 125 YVAICNPLRSTLTTRRIYKMGSLSVLRSAALLILPFLPKRPHYCRSHVLAHAYCGL 184
CY 186 DVMKACDDIRVNVVGLIYIISALIGDSLISFSTYLLIKTVLG-LTRPAQAKAFCTCV 244
DB 185 EIMKLACSSIIIVHVIYGLFVACTGVDSLLIFSTYLLIHAIVLGKRSRQERLRALMTICI 244
CY 245 SHVCAVFIFFVPIGISMVTRFSEKRDSPVLNANIYLLVPVNPVYGVTKETIROR 304
DB 245 SHICAVLFTFPMIGSLVRFSEHLPRIVHLMSTVYLLVPLMNPVYSINKQIROR 304
CY 305 ILRLP 309
DB 305 IIRKF 309
RESULT 19
O8VGZ6 MOUSE
ID O8VGZ6_MOUSE PRELIMINARY; PRT; 314 AA.
AC O8VGZ6;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, last annotation update)
DE Olfactory receptor MOR14-2 (Olfactory receptor Olfr561).
GN Name=Olfr561;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RL "The olfactory receptor gene superfamily of the mouse."; Nat. Neurosci. 5:124-133(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.;
RL "Different evolutionary processes shaped the mouse and human olfactory receptor gene families."; Hum. Mol. Genet. 11:535-546(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A., Walker M., Williams E.M., Trask B.J.;
RL "Odorant receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels."; Genome Biol. 4:R71-R71(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072994; AL60657.1; -; Genomic DNA.
DR EMBL; AY317676; AAP71055.1; -; Genomic DNA.
DR Ensembl; ENSMUSG00000051711; Mus musculus.
DR MGI; MGI:3030395; Olfr561.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.

DR Pfam; PF00001; 7cm 1; 1.
 DR PRINTS; PR00237; GPCRHOOPRN.
 DR PROSITE; PR00245; OLFACTORR.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KW Receptor.
 SQ SEQUENCE 314 AA; 35096 MW; 9F1016F8B1A040B9 CRC64;
 Query Match 54.0%; Score 875.5; DB 2; Length 314;
 Best Local Similarity 52.3%; Pred. No. 8.3e-58;
 Matches 162; Conservative 63; Mismatches 82; Indels 3; Gaps 2;
 QY 5 PGNSSA--TYFLIGLPGLEBAQFLAPLCSLYLVAVGNLTIIYVTEHSLHPM 62
 DB 2 PSFESAVPVFLTGIPGLGETHTWISIFPCGLVIAISGNMILFVITTESLHPM 61
 QY 63 YIFLCMLSGDILISTSMFPMALIFPNSTTIQPDACLDIPIAHISGMSVTLAMA 122
 DB 62 YIFLSMLSTFDIGLSTLVVLGIFPFWNVEISFDACIGMFIHGFTESSVLLVMA 121
 QY 123 FDRVVAICHLRHAATVLTLPRTKIGVAAVVGAALMAVLPFIKOLPFCRSNLSHSYC 182
 DB 122 FDRFALCNPLRKMILNHSKIIIVGFAIIRKTTALVPLLLKRLSFCSHVLSHC 181
 QY 183 LHODVWLACDDIRVNVVGLIVISAGLDSLISFSYLLIKTVGL-TRBAQAKAF 241
 DB 182 FHPDVMKLSGSDTRINSAGLAIVISTAGLDSVLILSVYLIIHSVLCIASKERRKAF 241
 QY 242 TCVSHVCAVPIFYPPFGLSMVHRFSKRDSPLPVILANITLVLPVPLNPIYGVTKKEI 301
 DB 242 TCVSHLAAVAFIYIPMISLSLHFRFGKAPPVHTLIANVLLIPVWNPPIYSVKTKQI 301
 QY 302 RQRIIRLRFV 311
 DB 302 RKAMLKVPV 311
 Db 302 RKAMLKVPV 311
 RESULT 20
 Q8VG22 MOUSE
 ID Q8VG22_MOUSE PRELIMINARY; PRT; 314 AA.
 AC Q8VG22;
 DT 01-MAR-2002 (Tremblrel. 20. Created)
 DT 01-MAR-2002 (Tremblrel. 20. Last sequence update)
 DT 01-FEB-2005 (Tremblrel. 29. Last annotation update)
 DB Olfactory receptor MOR30-1 (Olfactory receptor Olfr569).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21676863; PubMed=11802173;
 RA Zhang X., Firestein S.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RN Nat. Neurosci. 5:124-133(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
 RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
 RA Trask B.U.;
 RT "Different evolutionary processes shaped the mouse and human olfactory
 RT receptor gene families";
 RT Hum. Mol. Genet. 11:535-546(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-771;
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,

RA Walker M., Williams E.M., Trask B.U.;
 RT "Odorant receptor expressed sequence tags demonstrate olfactory
 RT expression of over 400 genes, extensive alternative splicing and unequal
 RT expression levels";
 RL Genome Biol. 4:R71-R71(2003).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072998; AL60661.1; -; Genomic DNA.
 DR EMBL; AY317684; AAP71059.1; -; Genomic DNA.
 DR EMBL; ENSMUSG0000062142; Mus musculus.
 DR MG1; MG1:3030403; Olfr569.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004984; F:olfactory receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007186; P:c-protein coupled receptor protein signaln. . .; IEA.
 DR GO; GO:0007185; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR000725; Olfact_receptor.
 DR PANTHER; PTHR11398; Olfact_receptor; 1.
 DR Pfam; PF00001; 7cm 1; 1.
 DR PRINTS; PR00237; GPCRHOOPRN.
 DR PROSITE; PR00245; OLFACTORR.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KW Receptor.
 SQ SEQUENCE 314 AA; 35578 MW; 718FEF2F351F669 CRC64;
 Query Match 53.9%; Score 873.5; DB 2; Length 314;
 Best Local Similarity 50.2%; Pred. No. 1.2e-57;
 Matches 155; Conservative 68; Mismatches 85; Indels 1; Gaps 1;
 QY 2 MDPNGSSATYFYLIGLPGLEBAQFLAPLCSLYLVAVGNLTIIYVTEHSLHPM 61
 DB 1 MVASSSSSHPLEFFMLGIFGLERYQFPIAPPCWMIYVLTGNTIILYIRIDHTLHP 60
 QY 62 MYFLCMLSGDILISTSMFPMALIFPNSTTIQPDACLDIPIAHISGMSVTLAM 121
 DB 61 MYFLALATLDTLVLSSTQPKMALIMFHSHEIBVACLIQVFFIHFASVSGLVMTM 120
 QY 122 AFDRYVACIPLRHAATVLTLPRTKIGVAAVVGAALMAVLPFIKOLPFCRSNLSHSY 181
 DB 121 ALDRYVACIPLRHSISLITTSVYIKGAAVVVGGLMVSPFCFMSMPCPKVPIQSY 180
 QY 182 CLHODVWLACDDIRVNVVGLIVISAGLDSLISFSYLLIKTVGL-TRBAQAKAF 240
 DB 181 CEMAVLACVCAQTRVNRGIGLVASVGFDIIVISVIVMILRAVLRLPSEARLAKAF 240
 QY 241 GTCVSHVCAVPIFYPPFGLSMVHRFSKRDSPLPVILANITLVLPVPLNPIYGVTKKE 300
 DB 241 GTCASHVCVILAFIYPLPFLTLTRFGHVPVAVHMFANFYLVPMLNPIYGVATKQ 300
 QY 301 IRORIIRLRF 309
 DB 301 IRDRIKRGF 309

Search completed: March 9, 2006, 08:29:14
 Job time : 234 secs

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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:29:29 ; Search time 46 Seconds
(without alignments)
571.541 Million cell updates/sec

Title: US-10-001-469A-2866
Perfect score: 1622
Sequence: 1 MWVDPMGNSSATRYFLIGL.....KEIKRRIILNFVHTASRP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PCOMB_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCOMB_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1619	99.8	318	2	US-09-759-143-920
2	1619	99.8	318	2	US-10-012-896-920
3	1617	99.7	317	2	US-09-680-728-2
4	1617	99.7	317	2	US-10-017-066A-2
5	979	60.4	320	2	US-09-439-313-527
6	979	60.4	320	2	US-09-636-215-527
7	979	60.4	320	2	US-09-685-166A-527
8	979	60.4	320	2	US-09-679-426-527
9	979	60.4	320	2	US-09-759-143-527
10	979	60.4	320	2	US-09-651-236-527
11	979	60.4	320	2	US-09-968-033C-4
12	979	60.4	320	2	US-09-657-279-527
13	979	60.4	320	2	US-10-012-896-527
14	977	60.2	320	2	US-09-680-728-3
15	977	60.2	320	2	US-10-017-066A-3
16	965.5	59.5	320	2	US-09-968-033C-2
17	964.5	59.5	320	1	US-08-465-980-2
18	964.5	59.5	320	1	US-09-053-303-2
19	964.5	59.5	320	2	US-09-339-115-2
20	964.5	59.5	320	2	US-09-680-728-4
21	964.5	59.5	320	2	US-10-017-066A-4
22	964.5	59.5	320	4	PCT-US95-07093-2
23	427.5	26.4	314	2	US-08-988-876-7
24	427.5	26.4	314	2	US-09-968-033C-5
25	413.5	25.5	340	2	US-09-546-986A-6
26	413.5	25.5	340	2	US-09-524-730-6
27	402.5	24.8	310	2	US-09-546-986A-2

28	402.5	24.8	310	2	US-09-524-730-2	Sequence 2, Appli
29	394.5	24.3	309	2	US-08-988-876-5	Sequence 8, Appli
30	387.5	23.9	334	2	US-09-546-986A-8	Sequence 8, Appli
31	387.5	23.9	334	2	US-09-524-730-8	Sequence 8, Appli
32	383	23.6	333	2	US-08-988-876-6	Sequence 46, Appli
33	374	23.1	313	2	US-09-465-901-48	Sequence 2, Appli
34	367	22.6	296	2	US-08-467-948A-2	Sequence 2, Appli
35	367	22.6	296	2	US-08-467-947A-2	Sequence 24, Appli
36	358.5	22.1	327	2	US-08-748-506-24	Sequence 3, Appli
37	357.5	22.0	247	1	US-08-465-980-3	Sequence 3, Appli
38	357.5	22.0	247	1	US-09-053-303-3	Sequence 3, Appli
39	357.5	22.0	247	2	US-09-339-115-3	Sequence 3, Appli
40	357.5	22.0	247	4	PCT-US95-07093-3	Sequence 3, Appli
41	357.5	22.0	316	1	US-08-827-291A-2	Sequence 2, Appli
42	355.5	21.9	284	1	US-08-118-270-61	Sequence 61, Appli
43	355.5	21.9	284	4	PCT-US93-08528-61	Sequence 61, Appli
44	354.5	21.9	321	2	US-08-748-506-20	Sequence 20, Appli
45	351.5	21.7	321	2	US-08-748-506-12	Sequence 12, Appli
46	348	21.5	321	2	US-08-748-506-18	Sequence 67, Appli
47	347	21.4	284	1	US-08-118-270-67	Sequence 67, Appli
48	347	21.4	284	4	PCT-US93-08528-67	Sequence 67, Appli
49	345.5	21.3	321	2	US-08-748-506-13	Sequence 13, Appli
50	345	21.3	321	2	US-08-748-506-10	Sequence 10, Appli
51	339.5	20.9	293	1	US-08-118-270-60	Sequence 60, Appli
52	339.5	20.9	293	4	PCT-US93-08528-60	Sequence 60, Appli
53	337.5	20.8	327	2	US-08-748-506-14	Sequence 14, Appli
54	335.5	20.7	277	1	US-08-118-270-62	Sequence 62, Appli
55	335.5	20.7	277	4	PCT-US93-08528-62	Sequence 62, Appli
56	332.5	20.5	327	2	US-08-748-506-22	Sequence 22, Appli
57	332.5	20.5	327	2	US-08-748-506-23	Sequence 23, Appli
58	329	20.3	277	1	US-08-118-270-68	Sequence 68, Appli
59	329	20.3	277	4	PCT-US93-08528-68	Sequence 68, Appli
60	329	20.3	321	2	US-08-748-506-11	Sequence 11, Appli
61	326	20.1	286	1	US-08-118-270-65	Sequence 65, Appli
62	326	20.1	286	4	PCT-US93-08528-65	Sequence 65, Appli
63	326	20.1	321	2	US-08-748-506-19	Sequence 19, Appli
64	320	19.7	273	1	US-08-118-270-63	Sequence 63, Appli
65	320	19.7	273	4	PCT-US93-08528-63	Sequence 63, Appli
66	320	19.7	274	1	US-08-118-270-69	Sequence 69, Appli
67	320	19.7	274	4	PCT-US93-08528-69	Sequence 69, Appli
68	318.5	19.6	275	1	US-08-118-270-66	Sequence 66, Appli
69	318.5	19.6	275	4	PCT-US93-08528-66	Sequence 66, Appli
70	310.5	19.1	269	1	US-08-118-270-64	Sequence 64, Appli
71	310.5	19.1	269	4	PCT-US93-08528-64	Sequence 64, Appli
72	286.5	18.3	331	2	US-09-546-986A-4	Sequence 4, Appli
73	296.5	18.3	331	2	US-09-524-730-4	Sequence 4, Appli
74	291	17.9	222	2	US-09-465-901-34	Sequence 34, Appli
75	285.5	17.6	222	1	US-08-467-948A-27	Sequence 27, Appli
76	285.5	17.6	222	2	US-08-467-947A-27	Sequence 27, Appli
77	283.5	17.1	223	2	US-09-465-901-40	Sequence 40, Appli
78	277.5	17.1	223	2	US-09-465-901-18	Sequence 18, Appli
79	268.5	16.6	223	2	US-09-465-901-26	Sequence 26, Appli
80	268.5	16.6	223	2	US-09-465-901-38	Sequence 38, Appli
81	268	16.5	222	2	US-09-465-901-44	Sequence 44, Appli
82	254.5	15.7	223	2	US-09-465-901-16	Sequence 16, Appli
83	253.5	15.6	223	2	US-09-465-901-12	Sequence 12, Appli
84	252.5	15.6	223	2	US-09-465-901-30	Sequence 30, Appli
85	250	15.4	224	2	US-09-465-901-36	Sequence 36, Appli
86	246.5	15.2	223	2	US-09-465-901-42	Sequence 42, Appli
87	246.5	15.2	223	2	US-09-465-901-32	Sequence 32, Appli
88	245.5	15.1	163	3	US-09-680-728-7	Sequence 7, Appli
89	236.5	14.6	163	2	US-10-017-066A-7	Sequence 7, Appli
90	236.5	14.6	163	2	US-09-465-901-24	Sequence 24, Appli
91	236.5	14.6	223	2	US-09-465-901-14	Sequence 14, Appli
92	233.5	14.3	223	2	US-09-465-901-20	Sequence 20, Appli
93	231.5	14.3	223	2	US-09-465-901-28	Sequence 28, Appli
94	231.5	14.3	223	2	US-09-465-901-22	Sequence 22, Appli
95	227.5	14.0	326	2	US-08-988-876-1	Sequence 1, Appli
96	215.5	13.3	326	2	US-09-759-143-925	Sequence 95, App
97	201	12.4	37	2	US-10-012-896-925	Sequence 95, App
98	201	12.4	177	2	US-08-748-506-21	Sequence 21, Appli
99	189.5	11.7	332	2	US-09-831-206-2	Sequence 2, Appli
100	189.5	11.7	332	2	US-09-831-206-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-09-759-143-920
; Sequence 920, Application US/09759143
; Patent No. 6800746
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-920

Query Match      99.8%; Score 1619; DB 2; Length 318;
Best Local Similarity 99.7%; Pred. No. 1e-139;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFLLIGLPGLEBAQFWLAFPLCSLYLVAIGNTTIYIVRTEHSLHE 60
DB 1 MMVDPNGNESSATYFLLIGLPGLEBAQFWLAFPLCSLYLVAIGNTTIYIVRTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAPRYYAICPLRHAATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAPRYYAICPLRHAATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
QY 121 YCHLQDVWKLACDDIRVVVYGLIYIISAIGDLSLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCHLQDVWKLACDDIRVVVYGLIYIISAIGDLSLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
DB 181 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
QY 241 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
DB 241 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
QY 301 IRRRIILRFHVATHASEP 318
DB 301 IRRRIILRFHVATHASEP 318
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RESULT 2
US-10-012-896-920
; Sequence 920, Application US/10012896
; Patent No. 6943236
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Basseols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-920

Query Match      99.8%; Score 1619; DB 2; Length 318;
Best Local Similarity 99.7%; Pred. No. 1e-139;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFLLIGLPGLEBAQFWLAFPLCSLYLVAIGNTTIYIVRTEHSLHE 60
DB 1 MMVDPNGNESSATYFLLIGLPGLEBAQFWLAFPLCSLYLVAIGNTTIYIVRTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAPRYYAICPLRHAATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAPRYYAICPLRHAATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
QY 121 YCHLQDVWKLACDDIRVVVYGLIYIISAIGDLSLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCHLQDVWKLACDDIRVVVYGLIYIISAIGDLSLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
DB 241 GTCVSHVCAVFIYVFPFGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
QY 301 IRRRIILRFHVATHASEP 318
DB 301 IRRRIILRFHVATHASEP 318

RESULT 3
US-09-680-728-2
; Sequence 2, Application US/09680728
; Patent No. 6790631
GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
```

APPLICANT: Daniel E. H. Afar
APPLICANT: Aya Jakobovits
APPLICANT: Mary Faris
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
TITLE OF INVENTION: UP-REGULATED IN PROSTATE CANCER AND USES THEREOF
FILE REFERENCE: 129,24US01
CURRENT APPLICATION NUMBER: US/09/680,728
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/157,902
PRIOR FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 317
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-680-728-2

Query Match 99.7%; Score 1617; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MVDPNNGESSATYFIILGLPGLBEAQFWLAFPLCSYLIANVLGNLTIIYVTRHSHAP 61
DB 1 MVDPNNGESSATYFIILGLPGLBEAQFWLAFPLCSYLIANVLGNLTIIYVTRHSHAP 60
QY 62 MYFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACLLQIPAIHSLSGMESTVLLAM 121
DB 61 MYFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACLLQIPAIHSLSGMESTVLLAM 120
QY 122 APDRYVAICHLRHATVLTLPRTVKIGVAAVRGALMAPLPVFIKQLPFCRSNIIISHSY 181
DB 121 APDRYVAICHLRHATVLTLPRTVKIGVAAVRGALMAPLPVFIKQLPFCRSNIIISHSY 180
QY 182 CLHQDVWKLACDDIRVNVVYGLIIVISAIGLDSLLISFSYLLILKTVLGLTREAOAKAFG 241
DB 181 CLHQDVWKLACDDIRVNVVYGLIIVISAIGLDSLLISFSYLLILKTVLGLTREAOAKAFG 240
QY 242 TCVSHVCAPVIFVYPPFGLSMVHRFSKRSDPLVILANIYLLVPPVLANPIVGVKTKEI 301
DB 241 TCVSHVCAPVIFVYPPFGLSMVHRFSKRSDPLVILANIYLLVPPVLANPIVGVKTKEI 300
QY 302 RORILRLFHVATHASEP 318
DB 301 RORILRLFHVATHASEP 317

RESULT 4
US-10-017-066A-2
Sequence 2, Application US/10017066A
Patent No. 6838258
GENERAL INFORMATION:
APPLICANT: Arthur B. Raitano
APPLICANT: Daniel E. H. Afar
APPLICANT: Aya Jakobovits
APPLICANT: Mary Faris
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
TITLE OF INVENTION: UP-REGULATED IN PROSTATE CANCER AND USES THEREOF
FILE REFERENCE: 511582002410
CURRENT APPLICATION NUMBER: US/10/017,066A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: US 09/680,728
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/157,902
PRIOR FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2
LENGTH: 317
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-017-066A-2

Query Match 99.7%; Score 1617; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MVDPNNGESSATYFIILGLPGLBEAQFWLAFPLCSYLIANVLGNLTIIYVTRHSHAP 61
DB 1 MVDPNNGESSATYFIILGLPGLBEAQFWLAFPLCSYLIANVLGNLTIIYVTRHSHAP 60
QY 62 MYFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACLLQIPAIHSLSGMESTVLLAM 121
DB 61 MYFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACLLQIPAIHSLSGMESTVLLAM 120
QY 122 APDRYVAICHLRHATVLTLPRTVKIGVAAVRGALMAPLPVFIKQLPFCRSNIIISHSY 181
DB 121 APDRYVAICHLRHATVLTLPRTVKIGVAAVRGALMAPLPVFIKQLPFCRSNIIISHSY 180
QY 182 CLHQDVWKLACDDIRVNVVYGLIIVISAIGLDSLLISFSYLLILKTVLGLTREAOAKAFG 241
DB 181 CLHQDVWKLACDDIRVNVVYGLIIVISAIGLDSLLISFSYLLILKTVLGLTREAOAKAFG 240
QY 242 TCVSHVCAPVIFVYPPFGLSMVHRFSKRSDPLVILANIYLLVPPVLANPIVGVKTKEI 301
DB 241 TCVSHVCAPVIFVYPPFGLSMVHRFSKRSDPLVILANIYLLVPPVLANPIVGVKTKEI 300
QY 302 RORILRLFHVATHASEP 318
DB 301 RORILRLFHVATHASEP 317

RESULT 5
US-09-439-313-527
Sequence 527, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 527
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-09-439-313-527
Query Match 60.4%; Score 979; DB 2; Length 320;
Best Local Similarity 59.5%; Pred. No. 2.1e-81;
Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;
QY 8 NBSATYFIILGLPGLBEAQFWLAFPLCSYLIANVLGNLTIIYVTRHSHAPMYFLC 67
DB 5 NHTAT-FVLIDIGPGLBEAQFWLAFPLCSYLIANVLGNLTIIYVTRHSHAPMYFLC 63
QY 68 MLSGIDILISTSSMPKMLAIFWFNSTTIQPDACLLQIPAIHSLSGMESTVLLAMAPDRYV 127

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Db      64 MLAIDLALSTSTMPKIALFWPDSREISFBACTQMFPIHALSAIBSTILLAMAFCRYV 123
Qy      128 AICHPRLHATVLTLPRTYKIGVAANVRGALMAPVPIKOLPFCRSNIISHSVCLHODV 187
Db      124 AICHPRLHAAVLTNTVTAQIGIVAVNRGSLFPFPLIKRLAFCHSNVLSHCYHODV 183
Qy      188 MCLACDDIRVVVVYGLIYVISAIGDSLISFSYLLILKTVLGL-TREBAKAKAGTCVSH 246
Db      184 MCLAVADTLPRVVYGLTALILVMGVDVWFISLSTYLLIRTVLQPSKSEBAKAGTCVSH 243
Qy      247 VCAVFIFVFPPIGLSMVHRFSKRDSPLVILANTYLLVPPVLANPIYGVYKTEIRORIL 306
Db      244 IGVTLAFVPLIGLSVHRFGNSLHPYRVVMGDIYLLPVPINPIYGAKTQKQIRTRVL 303
Qy      307 RLPHVA 312
Db      304 AMFKIS 309
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RESULT 6

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US-09-636-215-527
; Sequence 527, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, JIangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: JIang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 527
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-527
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Query Match      60.4%; Score 979; DB 2; Length 320;
Best Local Similarity 59.5%; Pred. No. 2.1e-81;
Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;
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Qy      8 NESAATYFILIGLGBEAOFWLAPPLCSYLLAVLGNLTITIIYVTRTSHSLHEPMYFLC 67
Db      5 NPTIAT-FVLLIGIGLKEKAFHWGFPPLSMYVAMFGNCIVFIVTRTERSLHAPMYFLC 63
Qy      68 MLSGIDILISTSSMPKUALFWFNSTTIQPDACILQIFAIHSLSGMESTVYLLAMAFPRYV 127
Db      64 MLAIDLALSTSTMPKIALFWPDSREISFBACTQMFPIHALSAIBSTILLAMAFCRYV 123
Qy      128 AICHPRLHATVLTLPRTYKIGVAANVRGALMAPVPIKOLPFCRSNIISHSVCLHODV 187
Db      124 AICHPRLHAAVLTNTVTAQIGIVAVNRGSLFPFPLIKRLAFCHSNVLSHCYHODV 183
Qy      188 MCLACDDIRVVVVYGLIYVISAIGDSLISFSYLLILKTVLGL-TREBAKAKAGTCVSH 246
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Db      184 MCLAVADTLPRVVYGLTALILVMGVDVWFISLSTYLLIRTVLQPSKSEBAKAGTCVSH 243
Qy      247 VCAVFIFVFPPIGLSMVHRFSKRDSPLVILANTYLLVPPVLANPIYGVYKTEIRORIL 306
Db      244 IGVTLAFVPLIGLSVHRFGNSLHPYRVVMGDIYLLPVPINPIYGAKTQKQIRTRVL 303
Qy      307 RLPHVA 312
Db      304 AMFKIS 309
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RESULT 7

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US-09-685-166A-527
; Sequence 527, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, JIangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: JIang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 527
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-527
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Query Match      60.4%; Score 979; DB 2; Length 320;
Best Local Similarity 59.5%; Pred. No. 2.1e-81;
Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;
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```
Qy      8 NESAATYFILIGLGBEAOFWLAPPLCSYLLAVLGNLTITIIYVTRTSHSLHEPMYFLC 67
Db      5 NPTIAT-FVLLIGIGLKEKAFHWGFPPLSMYVAMFGNCIVFIVTRTERSLHAPMYFLC 63
Qy      68 MLSGIDILISTSSMPKUALFWFNSTTIQPDACILQIFAIHSLSGMESTVYLLAMAFPRYV 127
Db      64 MLAIDLALSTSTMPKIALFWPDSREISFBACTQMFPIHALSAIBSTILLAMAFCRYV 123
Qy      128 AICHPRLHATVLTLPRTYKIGVAANVRGALMAPVPIKOLPFCRSNIISHSVCLHODV 187
Db      124 AICHPRLHAAVLTNTVTAQIGIVAVNRGSLFPFPLIKRLAFCHSNVLSHCYHODV 183
Qy      188 MCLACDDIRVVVVYGLIYVISAIGDSLISFSYLLILKTVLGL-TREBAKAKAGTCVSH 246
Db      184 MCLAVADTLPRVVYGLTALILVMGVDVWFISLSTYLLIRTVLQPSKSEBAKAGTCVSH 243
Qy      247 VCAVFIFVFPPIGLSMVHRFSKRDSPLVILANTYLLVPPVLANPIYGVYKTEIRORIL 306
Db      244 IGVTLAFVPLIGLSVHRFGNSLHPYRVVMGDIYLLPVPINPIYGAKTQKQIRTRVL 303
Qy      307 RLPHVA 312
Db      304 AMFKIS 309
```


QY 68 MLAGIDILISTSSMPKMLAIFWNSSTTIOPDACLQIFAIHSLSGMSTVLLAMAFDRYV 127
 DB 64 MLAGIDILISTSSMPKMLAIFWNSSTTIOPDACLQIFAIHSLSGMSTVLLAMAFDRYV 123
 QY 128 AICPPLHATVLTLPRTKIGVAAVVGAALMAPLPVFIKQLPFCRNSNIISHSYCLHODV 187
 DB 124 AICPPLHATVLTLPRTKIGVAAVVGAALMAPLPVFIKQLPFCRNSNIISHSYCLHODV 183
 QY 188 MCLACDDIRVVNVVGLIIVTISAGLDSLISFSTLLIKTVLGL-TREDAKAFGTCVSH 246
 DB 184 MCLACDDIRVVNVVGLIIVTISAGLDSLISFSTLLIKTVLGL-TREDAKAFGTCVSH 243
 QY 247 VCAVFIFYVPEFGISWVHRFSKRDSPPLYLANIYLLVPPVLPVYGVYKXIRORIL 306
 DB 244 IGVVLAIFYVPEFGISWVHRFSKRDSPPLYLANIYLLVPPVLPVYGVYKXIRORIL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

RESULT 13

US-10-012-896-527
 ; Sequence 527, Application US/10012896
 ; Patent No. 6943236
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Katos, Michael D.
 ; APPLICANT: Ketter, Marc W.
 ; APPLICANT: Scolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hurrell, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Baebols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Mantanebe, Yoshihiro
 ; APPLICANT: Meagher, Madeleine Joy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C27
 ; CURRENT APPLICATION NUMBER: US/10/012.896
 ; CURRENT FILING DATE: 2001-12-10
 ; NUMBER OF SEQ. ID NOS: 1011
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 527
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-012-896-527

Query Match 60.4%; Score 979; DB 2; Length 320;
 Best Local Similarity 59.5%; Pred. No. 2.1e-81;
 Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;

QY 8 NBSATYFIIIGLPGLEBAQFWLAFPLCSLYLAVLGNLTITTYIVRTHSHLHEPMYIFLC 67
 DB 5 NBSATYFIIIGLPGLEBAQFWLAFPLCSLYLAVLGNLTITTYIVRTHSHLHEPMYIFLC 63
 QY 68 MLAGIDILISTSSMPKMLAIFWNSSTTIOPDACLQIFAIHSLSGMSTVLLAMAFDRYV 127
 DB 64 MLAGIDILISTSSMPKMLAIFWNSSTTIOPDACLQIFAIHSLSGMSTVLLAMAFDRYV 123

DB 64 MLAGIDILISTSSMPKMLAIFWNSSTTIOPDACLQIFAIHSLSGMSTVLLAMAFDRYV 123
 QY 128 AICPPLHATVLTLPRTKIGVAAVVGAALMAPLPVFIKQLPFCRNSNIISHSYCLHODV 187
 DB 124 AICPPLHATVLTLPRTKIGVAAVVGAALMAPLPVFIKQLPFCRNSNIISHSYCLHODV 183
 QY 188 MCLACDDIRVVNVVGLIIVTISAGLDSLISFSTLLIKTVLGL-TREDAKAFGTCVSH 246
 DB 184 MCLACDDIRVVNVVGLIIVTISAGLDSLISFSTLLIKTVLGL-TREDAKAFGTCVSH 243
 QY 247 VCAVFIFYVPEFGISWVHRFSKRDSPPLYLANIYLLVPPVLPVYGVYKXIRORIL 306
 DB 244 IGVVLAIFYVPEFGISWVHRFSKRDSPPLYLANIYLLVPPVLPVYGVYKXIRORIL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

RESULT 14

US-09-680-728-3
 ; Sequence 3, Application US/09680728
 ; Patent No. 6790631
 ; GENERAL INFORMATION:
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Aya Jakodovits
 ; APPLICANT: Mary Faris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Douglas C. Saffran
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
 ; FILE REFERENCE: 129.24USU1
 ; CURRENT APPLICATION NUMBER: US/09/680.728
 ; CURRENT FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/157,902
 ; PRIOR FILING DATE: 1999-10-05
 ; NUMBER OF SEQ. ID NOS: 50
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Rat Protein
 US-09-680-728-3

Query Match 60.2%; Score 977; DB 2; Length 320;
 Best Local Similarity 59.5%; Pred. No. 3.3e-81;
 Matches 182; Conservative 53; Mismatches 69; Indels 2; Gaps 2;

QY 8 NBSATYFIIIGLPGLEBAQFWLAFPLCSLYLAVLGNLTITTYIVRTHSHLHEPMYIFLC 67
 DB 5 NBSATYFIIIGLPGLEBAQFWLAFPLCSLYLAVLGNLTITTYIVRTHSHLHEPMYIFLC 63
 QY 68 MLAGIDILISTSSMPKMLAIFWNSSTTIOPDACLQIFAIHSLSGMSTVLLAMAFDRYV 127
 DB 64 MLAGIDILISTSSMPKMLAIFWNSSTTIOPDACLQIFAIHSLSGMSTVLLAMAFDRYV 123
 QY 128 AICPPLHATVLTLPRTKIGVAAVVGAALMAPLPVFIKQLPFCRNSNIISHSYCLHODV 187
 DB 124 AICPPLHATVLTLPRTKIGVAAVVGAALMAPLPVFIKQLPFCRNSNIISHSYCLHODV 183
 QY 188 MCLACDDIRVVNVVGLIIVTISAGLDSLISFSTLLIKTVLGL-TREDAKAFGTCVSH 246
 DB 184 MCLACDDIRVVNVVGLIIVTISAGLDSLISFSTLLIKTVLGL-TREDAKAFGTCVSH 243
 QY 247 VCAVFIFYVPEFGISWVHRFSKRDSPPLYLANIYLLVPPVLPVYGVYKXIRORIL 306
 DB 244 IGVVLAIFYVPEFGISWVHRFSKRDSPPLYLANIYLLVPPVLPVYGVYKXIRORIL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

```
RESULT 15
US-10-017-066A-3
; Sequence 3, Application US/10017066A
; Patent No. 6838258
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel B.H. Afar
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Douglas C. Saffran
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
; TITLE OF INVENTION: UP-REGULATED IN PROSTATE CANCER AND USES THEREOF
; FILE REFERENCE: 51158202410
; CURRENT APPLICATION NUMBER: US/10/017,066A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US 09/680,728
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Rat Protein
US-10-017-066A-3

Query Match      60.2%; Score 977; DB 2; Length 320;
Best Local Similarity 59.5%; Pred. No. 3,3e-81;
Matches 182; Conservative 53; Mismatches 69; Indels 2; Gaps 2;

QY      8 NEEATYFIIIGLPGLEBAQFWLAPPLCSLYLIAVGNLTIIYVIRTEHSLHEPMYIFLC 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      5 NFRHAT-FMLIGIGLEBAHFMFGFPLSMYVAVALFGNCIVFIVRTERSLHAPMYIFLC 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      68 MLSGIDILISTSSMPKMLAIFMNSTTIQPDACLIQIPAIHSLSGMESTVLLMAFDRYV 127
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      64 MLAIDIALSTSTMPKIALTFMDSREITFPDACLQMFPIHLSAISTILLMAAFDRYV 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      128 AICPLRHATVLTLPRTVIGIAVAVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHODV 187
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      124 AICPLRHAAVLTNTVYQIGVALVYRSLFFPPLIKRLAFCHSVVLSHSCVHQDV 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      188 MCLACDDIRVNVVGLVITISAGLDSLLISPSYLLIKTVLGL-TREAQAKAFGTGVSH 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      184 MCLAVTDLPRNVVGLTALILVMGVDVFIISYFLIRAVLOLPSKSRAKAFGTGVSH 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      247 VCAVFIPVPPFISGMVRFPSKRDSPVLIANIYLLVPPVLPVIVGVTKERORIL 306
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      244 IGVLAFTVPLIGLSVVRFGNSLDPIVILMGDVLPLPVINPFIIGAKTKQIRKVL 303
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      307 RLFFVA 312
      : : : : :
DB      304 AMFKIS 309
      : : : : :

RESULT 16
US-09-968-033C-2
; Sequence 2, Application US/09968033C
; Patent No. 6824893
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: Human Prostate Specific G-Protein Receptor HPPA070
; FILE REFERENCE: PFI80B1
; CURRENT APPLICATION NUMBER: US/09/968,033C
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,275
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 09/339,115
```

```
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 09/053,303
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 08/465,980
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (192)
; OTHER INFORMATION: Xaa equals any amino acid
US-09-968-033C-2

Query Match      59.5%; Score 965.5; DB 2; Length 320;
Best Local Similarity 59.4%; Pred. No. 3,7e-80;
Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;

QY      16 ILIGLPGLEBAQFWLAPPLCSLYLIAVGNLTIIYVIRTEHSLHEPMYIFLCMLSGIDIL 75
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      12 VLIGIPGLEBAHFMFGFPLSMYVAVACGNCIVFIVRTERSLHAPMYIFLCMLAIDLA 71
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      76 ISTSMKMLAIFMNSTTIQPDACLIQIPAIHSLSGMESTVLLMAFDRYVAICPLRH 135
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      72 LSTSTMPKIALTFMFSREISIBACLTQMFPIHLSAISTILLMAAFDRYVAICPLRH 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      136 ATVTLPRTVIGIAVAVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHODVCLACDDI 195
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      132 AAVALNTVYQIGIAVAVRGSLFFPPLIKRLAFCHSVVLSHSCVHQDVMLAYADT 191
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      196 RVNVVGLIYIISAGLDSLLISPSYLLIKTVLGL-TREAQAKAFGTGVSHCAVFIFY 254
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      192 XENVVGLTALILVMGVDVFIISYFLIRVLOLPSKSRAKAFGTGVSHGVLAIFY 251
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      255 VPFISGMVRFPSKRDSPVLIANIYLLVPPVLPVIVGVTKERORILRLFFVA 312
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      252 VPLIGSVVRFGNSLHPIRVVWGDVILPLPVINPFIIGAKTKQIRKVLAMFKIS 309
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 17
US-08-465-980-2
; Sequence 2, Application US/08465980
; Patent No. 5756309
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Li, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPPA070
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,980
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
```


REFERENCE/DOCKET NUMBER: 325800-446
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-980-2

Query Match 59.5%; Score 964.5; DB 1; Length 320;
Best Local Similarity 59.4%; Pred. No. 4.5e-80;
Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;

QY 16 ILIGLPGLEAQAFLAPLCSLYLAVLGNLTIIYVTEHSLHEPMYFLCMLSGDIL 75
DB 12 VLIGIPGLEKAHFWGVGFLSMYVAMGNCIVFIYRTSLHAPYFLCMLAIDL 71
QY 76 ISTSMPEKMLAIFWNSSTTIOFDACLIQIPAIHSLSGMESTVLLAMAFDRYVAICHPLRH 135
DB 72 LSTSTMPKIALLPFDSREISIEBCLTQMPFIHALSAIBSTIILAMAFDRYVAICHPLRH 131
QY 136 ATVLTLPRTKIGVAAVVRGAALMAPLPVFIKOLPFCRSNLSHSCYCHODVMKLAODI 195
DB 132 AAVANTVTAGIGVAVVRGSLPFFPLPLIKRLAFCHSNVLSHSCYCHODVMKLAAYDT 191
QY 196 RVNVVGLIYIISAIGDSLISPSYLLIKTVLGL-TREAQAKAFGTCVSHVCAVPIFY 254
DB 192 LPNVVGLTALLWAGDVWFISLSTPLIIRTVQLPSKERAFAFGTCVSHIGVLAIFY 251
QY 255 VPFGLSMWRHFRSGRDSPLPVILANTYLLVPVLANPIYGVKTKETRQRLRLPHVA 312
DB 252 VPLIGLSVHRFGNSLHPYRVVWGDYLLPLPVINPIYGAKTKQIRTVLAMEFKIS 309

RESULT 18

US-09-053-303-2
Sequence 2, Application US/09053303
Patent No. 5948890
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,303
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-053-303-2

Query Match 59.5%; Score 964.5; DB 1; Length 320;
Best Local Similarity 59.4%; Pred. No. 4.5e-80;
Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;

QY 16 ILIGLPGLEAQAFLAPLCSLYLAVLGNLTIIYVTEHSLHEPMYFLCMLSGDIL 75
DB 12 VLIGIPGLEKAHFWGVGFLSMYVAMGNCIVFIYRTSLHAPYFLCMLAIDL 71
QY 76 ISTSMPEKMLAIFWNSSTTIOFDACLIQIPAIHSLSGMESTVLLAMAFDRYVAICHPLRH 135
DB 72 LSTSTMPKIALLPFDSREISIEBCLTQMPFIHALSAIBSTIILAMAFDRYVAICHPLRH 131
QY 136 ATVLTLPRTKIGVAAVVRGAALMAPLPVFIKOLPFCRSNLSHSCYCHODVMKLAODI 195
DB 132 AAVANTVTAGIGVAVVRGSLPFFPLPLIKRLAFCHSNVLSHSCYCHODVMKLAAYDT 191
QY 196 RVNVVGLIYIISAIGDSLISPSYLLIKTVLGL-TREAQAKAFGTCVSHVCAVPIFY 254
DB 192 LPNVVGLTALLWAGDVWFISLSTPLIIRTVQLPSKERAFAFGTCVSHIGVLAIFY 251
QY 255 VPFGLSMWRHFRSGRDSPLPVILANTYLLVPVLANPIYGVKTKETRQRLRLPHVA 312
DB 252 VPLIGLSVHRFGNSLHPYRVVWGDYLLPLPVINPIYGAKTKQIRTVLAMEFKIS 309

RESULT 19

US-09-339-115-2
Sequence 2, Application US/09339115
Patent No. 6372891
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/053,303
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-339-115-2

Query March 59.5%; Score 964.5; DB 2; Length 320;
Best Local Similarity 59.4%; Pred. No. 4,5e-80;

Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;

QY 16 ILIGLPGLEAQAFLAPLCSLYLAVLGNLTIIYVTEHSLHBPYIFLCMTSGIDIL 75
DB 12 VLIGLPGLEKAHFWGFPILSMYVAMGNCIVIVTERSLHAPYILFLCMLAIDLA 71
QY 76 ISTSMPPKMLAIFWNSSTTIQPDACLIQIPAIHSLSGMESTVLLAMAFDRYVAICHPLRH 135
DB 72 LSTSTMPKILALFWPDSREISIEACTQMPFIHALSAESTILLAMAFDRYVAICHPLRH 131
QY 136 ATVLTLPVTKIGVAAYVRGALMALPVPFIKQLPFCRSNIISSHSCYCLHODVMKLAADDI 195
DB 132 AAVLANTVTQAQIGIAVAVRGSLFFPPLPLIKRLAFCHSNVLSHSYCVHODVMKLAAYDT 191
QY 196 RNVVYGLIYIISAIGDSLISFSYLLIKTVLGL-TREAQAKAFGTCVSHVCAVPIFY 254
DB 192 LPNVYGLTALLVWGVDVMPISLSYFLIRTVQLPSSKSRAKAFGTCVSHIGVLAIFY 251
QY 255 VPFGLSMVHRFSKRDSPLPVILANIYLLVPPVLPVIVYGVKTEIRORILRLFHVA 312
DB 252 VPLIGLSVHRFGNSLHPRIVRVWMDIYLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309

RESULT 20

US-09-680-728-4
Sequence 4, Application US/09680728
Patent No. 6790631

GENERAL INFORMATION:

APPLICANT: Arthur B. Raitano
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
APPLICANT: Mary Faris
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: 129.24USU1
CURRENT FILING DATE: 2000-10-05
PRIOR FILING DATE: 1999-10-05
CURRENT APPLICATION NUMBER: 60/157,902
PRIOR APPLICATION NUMBER: 60/157,902
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 320
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-680-728-4

Query Match 59.5%; Score 964.5; DB 2; Length 320;
Best Local Similarity 59.4%; Pred. No. 4,5e-80;

Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;

QY 16 ILIGLPGLEAQAFLAPLCSLYLAVLGNLTIIYVTEHSLHBPYIFLCMTSGIDIL 75
DB 12 VLIGLPGLEKAHFWGFPILSMYVAMGNCIVIVTERSLHAPYILFLCMLAIDLA 71
QY 76 ISTSMPPKMLAIFWNSSTTIQPDACLIQIPAIHSLSGMESTVLLAMAFDRYVAICHPLRH 135
DB 72 LSTSTMPKILALFWPDSREISIEACTQMPFIHALSAESTILLAMAFDRYVAICHPLRH 131
QY 136 ATVLTLPVTKIGVAAYVRGALMALPVPFIKQLPFCRSNIISSHSCYCLHODVMKLAADDI 195

DB 132 AAVLANTVTQAQIGIAVAVRGSLFFPPLPLIKRLAFCHSNVLSHSYCVHODVMKLAAYDT 191
QY 196 RNVVYGLIYIISAIGDSLISFSYLLIKTVLGL-TREAQAKAFGTCVSHVCAVPIFY 254
DB 192 LPNVYGLTALLVWGVDVMPISLSYFLIRTVQLPSSKSRAKAFGTCVSHIGVLAIFY 251
QY 255 VPFGLSMVHRFSKRDSPLPVILANIYLLVPPVLPVIVYGVKTEIRORILRLFHVA 312
DB 252 VPLIGLSVHRFGNSLHPRIVRVWMDIYLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309

Search completed: March 9, 2006, 08:30:51
Job time : 47 secs